GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 13, 2004, 09:24:53 ; Search time 7717 Seconds
                                         (without alignments)
                                         12162.347 Million cell updates/sec

Title: US-10-015-391A-276
Perfect score: 3143
Sequence: 1 gggctgaggcactgagagac.........aaatataaggcttaaaaaaa 3143

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                 1: em_estba:*
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                 16: em_estom:*
                 17: em_gss_hum:*
                 18: em_gss_inv:*
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                 20: em_gss_vrt:*
                 21: em_gss_fun:*
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                 23: em_gss_mus:*
                 24: em_gss_pro:*
                 25: em_gss_rod:*
                 26: em_gss_phg:*
                 27: em_gss_vrl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1874	59.6	2172	29	AY402621	AY402621 Homo sapi
	2	1765.4	56.2	2133	29	AY402622	AY402622 Pan trogl
	3	1747.4	55.6	3206	11	AK077976	AK077976 Mus muscu
	4	1701.4	54.1	3086	11	AK035918	AK035918 Mus muscu
	5	1372.2	43.7	2172	29	AY402623	AY402623 Mus muscu
c	6	950.6	30.2	1114	13	BX367242	BX367242 BX367242
c	7	927.8	29.5	1201	13	BX363741	BX363741 BX363741
c	8	874.4	27.8	922	13	BX350606	BX350606 BX350606
	9	856.6	27.3	926	13	BX328255	BX328255 BX328255
	10	849.2	27.0	1201	13	BX384966	BX384966 BX384966
	11	827.4	26.3	974	13	BQ057192	BQ057192 AGENCOURT
	12	822.2	26.2	960	13	BX390196	BX390196 BX390196
c	13	779.8	24.8	797	14	CB243787	CB243787 UI-CF-FN0
	14	775	24.7	801	13	BX112994	BX112994 BX112994
	15	769.8	24.5	912	13	BQ883972	BQ883972 AGENCOURT
	16	768	24.4	1201	13	BX376660	BX376660 BX376660
	17	757.6	24.1	892	14	CD107028	CD107028 AGENCOURT
	18	748.6	23.8	951	13	BQ056228	BQ056228 AGENCOURT
	19	696.6	22.2	775	9	AU122156	AU122156 AU122156
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	21	681	21.7	1066	12	BM806752	BM806752 AGENCOURT
	22	673	21.4	1090	13	BX367243	BX367243 BX367243
	23	661.8	21.1	666	12	BG684636	BG684636 602635914
	24	650	20.7	925	13	BQ937439	BQ937439 AGENCOURT
c	25	627.4	20.0	640	14	CA311774	CA311774 UI-CF-FN0
c	26	612	19.5	624	12	BM666780	BM666780 UI-E-CL1-
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	28	598.6	19.0	621	10	AW965845	AW965845 EST377918
c	29	598.4	19.0	634	13	BU632880	BU632880 UI-H-FE1-
c	30	594	18.9	618	13	BU686374	BU686374 UI-CF-DU1
	31	585.2	18.6	881	13	BQ960065	BQ960065 AGENCOURT
	32	579.2	18.4	720	14	CA315771	CA315771 UI-M-FW0-
	33	557.8	17.7	796	13	BU052878	BU052878 UI-M-FC0-
	34	552.6	17.6	917	14	CA454892	CA454892 AGENCOURT
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RESULT 1
AY402621

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DEFINITION  Homo sapiens HCM1285 gene, VIRTUAL TRANSCRIPT, partial sequence,
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ACCESSION   AY402621
VERSION     AY402621.1  GI:39758607
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2172)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
  PUBMED    14671302
REFERENCE   2  (bases 1 to 2172)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
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   Matches 1874;  Conservative    0;  Mismatches  298;  Indels    0;  Gaps    0;
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Qy     165 CTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGGAGGCGGGCAGGGGCCCATGCCC 224
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Db      61 CTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGGAGGCGGGCAGGGGCCCATGCCC 120
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Qy     225 AGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGC 284
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Qy     285 CTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCT 344
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Db     181 CTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCT 240

Qy     345 CGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATG 404
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Qy     405 ATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAAT 464
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Qy     465 GAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTAC 524
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Qy     645 GCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAAC 704
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Qy     705 TTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACC 764
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Qy     765 GACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACC 824
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Qy     825 CAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTC 884

Db     721 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 780

Qy     885 CACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAG 944

Db     781 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 840

Qy     945 AAGAAGTGGACCACCTTCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCC 1004

Db     841 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 900

Qy    1005 TTCAACGTCATCCGCCACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATC 1064

Db     901 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 960

Qy    1065 TACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCC 1124
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Qy   1125 TTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAA 1184
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Qy      2145 TGGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATC 2204
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Qy      2205 ATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAG 2264
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Db      2101 ATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAG 2160

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RESULT 2
AY402622

LOCUS	AY402622	2133 bp DNA linear GSS 12-DEC-2003
DEFINITION	Pan troglodytes HCM1285 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.	
ACCESSION	AY402622	
VERSION	AY402622.1 GI:39758608	
KEYWORDS	GSS.	
SOURCE	Pan troglodytes (chimpanzee)	
ORGANISM	Pan troglodytes	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.	
REFERENCE	1 (bases 1 to 2133)	
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.	
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios	
JOURNAL	Science 302 (5652), 1960-1963 (2003)	
PUBMED	14671302	
REFERENCE	2 (bases 1 to 2133)	
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.	
TITLE	Direct Submission	
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA	
COMMENT	This sequence was made by sequencing genomic exons and ordering	

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ORIGIN

  Query Match            56.2%;  Score 1765.4;  DB 29;  Length 2133;
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Qy      225 AGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGC 284
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Db      121 AGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGC 180

Qy      285 CTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCT 344
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Qy      345 CGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATG 404
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Qy      405 ATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAAT 464
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Db      301 ATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAAT 360

Qy      465 GAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTAC 524
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Qy      525 ACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTAC 584
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Db      541 GCTCACAAGCATACGGCTGTCTTGGTGGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 600

Qy      705 TTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACC 764
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Db      601 NTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACC 660
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Qy    765 GACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACC 824
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Db    661 GACAACTTCCTCCGCTGGCTGCATCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 720

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Qy   1065 TACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCC 1124
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Qy   1185 ACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCA 1244
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Qy   1305 CAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTG 1364
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Qy   1365 GAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACA 1424
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACA 1320

Qy   1425 GGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATT 1484
          ||||||  |||||||||||||||||||||||||||||||||||||||||||||||    ||
Db   1321 GGGTCGNTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGANNNNNTT 1380

Qy   1485 CAGCTGTTCCCTGACCCTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCA 1544
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Qy    1605  GAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCC  1664
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Qy    1965  CTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTG  2024
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RESULT 3
AK077976
LOCUS   AK077976   3206 bp   mRNA   linear   HTC 18-SEP-2003
DEFINITION Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
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            immunoglobulin domain (Ig), transmembrane domain (TM) and short
            cytoplasmic domain, (semaphorin) 4A, full insert sequence.
ACCESSION   AK077976
VERSION   AK077976.1 GI:26097602
KEYWORDS   HTC; CAP trapper.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus

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                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
    TITLE   High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
                Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
    TITLE   Normalization and subtraction of cap-trapper-selected cDNAs to
                prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
                Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
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                Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
                Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
    TITLE   RIKEN integrated sequence analysis (RISA) system--384-format
                sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
                FANTOM Consortium.
    TITLE   Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
                Group Phase I & II Team.
    TITLE   Analysis of the mouse transcriptome based on functional annotation
                of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 3206)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
                Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
                Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
                Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
                Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
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                Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
                Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
                Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
                Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
                Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
                Muramatsu,M. and Hayashizaki,Y.
    TITLE   Direct Submission
  JOURNAL   Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
                Physical and Chemical Research (RIKEN), Laboratory for Genome
                Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
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                  RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
                  Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
                  URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                  Fax:81-45-503-9216)
COMMENT           cDNA library was prepared and sequenced in Mouse Genome
                  Encyclopedia Project of Genome Exploration Research Group in Riken
                  Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                  Division of Experimental Animal Research in Riken contributed to
                  prepare mouse tissues.
                  Please visit our web site for further details.
                  URL:http://genome.gsc.riken.go.jp/
                  URL:http://fantom.gsc.riken.go.jp/.
FEATURES          Location/Qualifiers
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                  domain (TM) and short cytoplasmic domain, (semaphorin) 4A
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     polyA_site   3206
                  /note="putative"
ORIGIN

  Query Match              55.6%;  Score 1747.4;  DB 11;  Length 3206;
  Best Local Similarity    76.7%;  Pred. No. 0;
  Matches 2355;  Conservative    0;  Mismatches  621;  Indels  95;  Gaps  14;


Qy      75 GAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCCC 134
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Db     194 GAACCATCTGGTGACCATCTCAGGCTGACCATGGCCCTACCATCCCTGGGCCAGGACTCA 253

Qy     135 TGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGCTGCCGACGACGACC 194
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Qy     195 GCGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATGCAGGGGATGAACGT 254
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Qy    315 GGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAG 374
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Qy    375 GATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAAG 434
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Qy    915 AATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCCAG 974
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Db   2231 CGGAGCTTCCATGGCTGCCCAGCGGTCCTACTGGCCCCATTTTCTCATCGTTACCGTCCT 2290

Qy   2174 CTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACT 2233
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Db   2291 CCTGGCCATCGTGCTCCTGGGAGTGCTCACTCTCCTCCTCGCTTCCCCACTGGGGGCGCT 2350

Qy   2234 CCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTT 2293
           |||||||||| ||||||||||||||||||| || |||| ||| |||| ||||| || |
Db   2351 GCGGGCTCGGGGTAAGGTTCAGGGCTGTGGGATGCTGCCCCCCAGGGAAAAGGCTCCACT 2410

Qy   2294 AAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGA 2353
           ||||| || || ||||||||| |    ||||||| |||||||||||||||||| || ||
Db   2411 GAGCAGGGACCAGCACCTCCAGCCCTCCAAGGACCACAGGACCTCTGCCAGTGACGTAGA 2470

Qy   2354 CGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCT- 2412
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Db   2471 TGCCGACAACAACCATCTGGGCGCCGAAGTGGCTTAAACAGGGACACAGATCCGCAGCTG 2530

Qy   2413 -GCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATG 2471
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Db   2531 AGCAGAGCAAGCCACTGGCCTTGTTGGCTATGC--------------------------- 2563

Qy   2472 ACAGCAGCACAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACT 2531
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Db   2564 ----CAGGCACAGTGCCACTCTGACCAGGGTAGGAGGCTCTCCTGCTAACGTGTGTCACC 2619

Qy   2532 GATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACC 2591
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Qy   2652 TGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAG 2711
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Qy   2772 CATCTAAACAATCATATGCTA-------ACATGCCACTCCTGGAAACTCCACTCT----G 2820
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Qy   2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTC-TCCCAGGGTCATGCAGGGATCTGCTCC 2879
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Qy      2880 CTCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTG 2939
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Db      2943 CTTGTGTTTCCTTTACCAGTCATGCCATACTGTTT---GGGAAGTCATCTCTGAAGTCTA 2999

Qy      2940 ACCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCT---TCTGCCCTGGC-AG 2995
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Db      3000 ACCACCTTCCTTCTTGCTTCAGTTTGGACAGATTGTTATTATTGTCTCTGCCCTGGCTAG 3059

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Db      3060 AATGGGGGGCATAATCTGAGCCTTGTTCCCTTGTCCAGTGTGGCTGACCCTTGACCTCTT 3119

Qy      3056 CCCCCTCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTT 3115
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Db      3120 --CCTTCCTCCTCCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCACAGACAATTTATTT 3177

Qy      3116 TTTATTAAAAA 3126
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RESULT 4
AK035918
LOCUS       AK035918              3086 bp     mRNA      linear      HTC 19-SEP-2003
DEFINITION  Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length
            enriched library, clone:9630018D15 product:sema domain,
            immunoglobulin domain (Ig), transmembrane domain (TM) and short
            cytoplasmic domain, (semaphorin) 4A, full insert sequence.
ACCESSION   AK035918
VERSION     AK035918.1  GI:26084904
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
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                 Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE   RIKEN integrated sequence analysis (RISA) system--384-format
                 sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
   MEDLINE   20530913
    PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
                 FANTOM Consortium.
  TITLE   Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
                 Group Phase I & II Team.
  TITLE   Analysis of the mouse transcriptome based on functional annotation
                 of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6 (bases 1 to 3086)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
                 Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
                 Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
                 Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
                 Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
                 Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
                 Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
                 Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
                 Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
                 Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
                 Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
                 Muramatsu,M. and Hayashizaki,Y.
  TITLE   Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
                 Physical and Chemical Research (RIKEN), Laboratory for Genome
                 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
                 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
                 Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
                 URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                 Fax:81-45-503-9216)
COMMENT   cDNA library was prepared and sequenced in Mouse Genome
                 Encyclopedia Project of Genome Exploration Research Group in Riken
                 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                 Division of Experimental Animal Research in Riken contributed to
                 prepare mouse tissues.
                 Please visit our web site for further details.
                 URL:http://genome.gsc.riken.go.jp/
                 URL:http://fantom.gsc.riken.go.jp/.
FEATURES   Location/Qualifiers
     source   1. .3086
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                          (MGD|MGI:107560, GB|NM_013658, evidence: BLASTN, 99%,
                          match=2517)"
            polyA_signal  3062. .3067
                          /note="putative"
            polyA_site    3086
                          /note="putative"
      ORIGIN

        Query Match            54.1%;   Score 1701.4;   DB 11;   Length 3086;
        Best Local Similarity  75.2%;   Pred. No. 0;
        Matches 2364;  Conservative    0;  Mismatches  637;  Indels  141;  Gaps    14;

      Qy      50 AACGCAGCGGCATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGC 109
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      Db       4 AACCCAGAAAGTGCCTGTTTCCTCAGAACCATCTGGTGACCATCTCAGGCTGACCATGGC 63

      Qy     110 CCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCT 169
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      Db      64 CCTACCATCCCTGGGCCAGGACTCATGGAGTCTCCTGCGTGTTTTTTCTTCCAACTCTT 123

      Qy     170 TCAGCTGCTGCTGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGT 229
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      Qy     230 CAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCA 289
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      Qy     290 GGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGA 349
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      Qy     350 AGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACC 409
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      Qy     470 ACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTG 529
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      Qy     530 CGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATT---------------------- 566
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      Db     484 TGGGACCTTTGCCTTCAGCCCTGCCTGTACCTTCATTACGTGCGACCCTGGCATTCTGGG 543

      Qy     567 ----------------------GAACTTCAAGATTCCTACCTGTTGCCCATCTCGGAG 602
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Qy    603  GACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCT   662
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Db    604  GACAAGGTCATGGACGGGAAGGGCCAAAGCCCCTTTGACCCTGTTCACAAGCACACAGCT   663

Qy    663  GTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCC   722
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Db    664  GTCTTGGTCGATGGGATGCTTTATTCCGGCACCATGAACAACTTCCTGGGCAGCGAGCCC   723

Qy    723  ATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCTGG   782
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Qy    783  CTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTC   842
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Qy    843  TTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCT   902
           ||  ||||||||||||||||||||||||||||||||||  ||| | | |||  |||||||||
Db    844  TTTGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAAGAGCTGTATATATCCAGGGTGGCT   903

Qy    903  AGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTC   962
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Db    904  CAAGTCTGCAAGAACGACGTGGGCGGTGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTC   963

Qy    963  CTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCAC   1022
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Qy    1083 CAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATT   1142
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Qy    1143 GAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTACT   1202
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Db    1144 GAGCGAGTCTTTAAAGGGAAGTACAAGGAGCTGAACAAGGAGACCTCCCGCTGGACCACT   1203

Qy    1203 TATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTGAT   1262
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Db    1204 TACCGGGGGCTCAGAGGTCAGCCCGAGGCCAGGCAGTTGCTCCATGGGCCCCTCCTCTGAC   1263

Qy    1263 AAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCC   1322
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Qy    1383 GATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGCT   1442
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Qy      2283 AAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCC 2342
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Db    2281 AAGGCTCCACTGAGCAGGGACCAGCACCTCCAGCCCTCCAAGGACCACAGGACCTCTGCC 2340

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Db    2341 AGTGACGTAGATGCCGACAACAACCATCTGGGCGCCGAAGTGGCTTAAACAGGGACACAG 2400

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Qy    2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580
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Db    2490 CGTGTGTCACCTACAGCACCCAGTAGGT-----------------CCTCCCCTGTGGGAC 2532

Qy    2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640
            || ||||| | |       || ||| |||                 ||| ||||| |
Db    2533 TCTCTTCTGCAAGCACATTGGGCTGTCT-------------------CCATACCTGTACT 2573

Qy    2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700
            |   |||  |  |  | | || ||| ||| | ||| || || ||   ||| | |||||
Db    2574 TGTGCTGTGACAGGAAGAGCCAGACAGGTTTCTTTGATTTTGATTGACCCAAGAGCCCTC 2633

Qy    2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760
            | | ||||| |       || || |   ||| ||     |   | ||| ||  |||| |
Db    2634 CTGTAACAAACGTGCTCCAGGAGACCATGAAAGGTGTGGCTGTCTGGGATTCTGTGGTGA 2693

Qy    2761 TGAACACCAAACATCTAAACAATCATATGCTA-------ACATGCCACTCCTGGAAACTC 2813
            ||| | || |||| | ||| |    |||| | | ||| |
Db    2694 CAAAC-CTAAGCATCCGAGCAAGCTGGGGCTATTCCTGCAAACTCCATCCTGAACGCTGT 2752

Qy    2814 CACTCT----GAAGCTGCCGCTTTGGACACCAACACTCCCTTC-TCCCAGGGTCATGCAG 2868
            ||||||     | ||||||| |||||| |||||| | | |||| | |||||| |   |
Db    2753 CACTCTAGAAGCAGCTGCTGCTTTGAACACCAGCCCACCCTCCTTCCCAAGAGTCTCTAT 2812

Qy    2869 GGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTT 2928
            ||| || |||| || |||| |||||||||||| |||     ||| | |||||| |
Db    2813 GGAGTTGGCCCCTTGTGTTTCCTTTACCAGTCATGCCATACTGTTT---GGGAAGTCATC 2869

Qy    2929 CCTGAAGTCTGACCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCT---TCT 2985
            |||||||| ||||||||| |||||||||||||||| || |||| | | || | |||
Db    2870 TCTGAAGTCTAACCACCTTCCTTCTTGCTTCAGTTTGGACAGATTGTTATTATTGTCTCT 2929

Qy    2986 GCCCTGGC-AGAATGGCAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACC 3044
            ||||||||| |||||||   || ||||||||||||| ||| ||   |   | |||||||
Db    2930 GCCCTGGCTAGAATGGGGGGGCATAATCTGAGCCTTGTTCCCTTGTCCAGTGTGGCTGACC 2989

Qy    3045 CCTTCACCTCTCCCCCTCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAG 3104
            || | | | ||  ||  | |||||||| ||||||||||||||||||||||||||||| ||
Db    2990 CTTGACCTCTT--CCTTCCTCCTCCCTTTGTTTGGGGATTCAGAAAACTGCTTGTCACAG 3047

Qy    3105 ACTGTTTATTTTTTATTAAAAA 3126
            ||  ||||||||||||||||||
Db    3048 ACAATTTATTTTTTATTAAAAA 3069
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RESULT 5
AY402623

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LOCUS          AY402623                2172 bp    DNA      linear   GSS 12-DEC-2003
DEFINITION  Mus musculus HCM1285 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY402623
VERSION     AY402623.1  GI:39758609
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 2172)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
  PUBMED    14671302
REFERENCE   2  (bases 1 to 2172)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .2172
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
     gene            <1. .>2172
                     /locus_tag="HCM1285"
ORIGIN
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Query Match              43.7%;  Score 1372.2;  DB 29;  Length 2172;
Best Local Similarity    71.9%;  Pred. No. 0;
Matches 1560;  Conservative    0;  Mismatches  611;  Indels    0;  Gaps    0;
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Qy    105 ATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAA 164
          ||||||||| ||| ||||||||| |||| | ||||| |||||| |  |||| |||||||||
Db      1 ATGGCCCTACCATCCCTGGGCCAGGACTCATGGAGTCTCCTGCGTGTTTTTTTCTTCCAA 60

Qy    165 CTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGGAGGCGGGCAGGGGCCCATGCCC 224
          ||  |  | ||||||     | | |  |  |  | |||  || || ||||||||||||||||
Db     61 CTCTTCCTGCTGCCATCACTGCCACCTGCTTCTGGGACTGGTGGTCAGGGGCCCATGCCC 120

Qy    225 AGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGC 284
          ||  |||| |||| |||| || || |  |     |||||| || |||||||||||| || |||
Db    121 AGAGTCAAATACCATGCTGGAGACGGGCACAGGGCCCTCAGCTTCTTCCAACAAAAGGC 180
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Qy    285 CTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCT 344
          ||||   ||  |||||||||  ||||||||||||||     ||||| || |||||||| ||||||||||
Db    181 CTCCGAGACTTTGACACGCTGCTCCTGAGTGACGATGGCAACACTCTCTATGTGGGGGCT 240

Qy    345 CGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATG 404
          |||||  |||   | |||||||||| |||||||| |  ||||||    |||| ||||||||||||||||||||
Db    241 CGAGAGGCCGTCCTGGCCTTGAATATCCAGAACCCAGGAATCCCAAGGCTAAAGAACATG 300

Qy    405 ATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAAT 464
          |||||  ||||||||||||||  ||||||||||| |||||||||    |||||||||||||||||||||||||||||||||
Db    301 ATACCCTGGCCAGCCAGTGAGAGAAAAAAGACCGAATGTGCCTTTAAGAAGAAGAGCAAT 360

Qy    465 GAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTAC 524
          ||||||||||||||||||||||  |||||||||| |||||||||||  || || |||||
Db    361 GAGACACAGTGTTTCAACTTCATTCGAGTCCTGGTCTCTTACAATGCTACTCACCTCTAT 420

Qy    525 ACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTAC 584
          ||||  || ||||| |||||||||||||||| ||||||||||||||||||||||||| |
Db    421 GCCTGTGGGACCTTTGCCTTCAGCCCTGCCTGTACCTTCATTGAACTCCAAGATTCCTC 480

Qy    585 CTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCC 644
          ||||||||||||| |   |||||||||||||||| || || |||||||||||||||||||||||||||||||||
Db    481 CTGTTGCCCATCTTGATAGACAAGGTCATGGACGGGAAGGGCCAAAGCCCCTTTGACCCT 540

Qy    645 GCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAAC 704
          | ||||||||| || ||||||||||| |||||||||||| ||||| || || |||||||||
Db    541 GTTCACAAGCACACAGCTGTCTTGGTCGATGGGATGCTTTATTCCGGCACCATGAACAAC 600

Qy    705 TTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGATCCCAGCCTGTCCTCAAGACC 764
          |||||||||||| ||||||||||||||||||| ||||||||||||||||||||| ||||||||
Db    601 TTCCTGGGCAGCGAGCCCATCCTGATGCGGACACTGGATCCCAGCCTGTTCTCAAGACT 660

Qy    765 GACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACC 824
          |||| |||| | |||||||||||||||
Db    661 GACATCTTCTTACGCTGGCTGCACGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 720

Qy    825 CAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTC 884

Db    721 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 780

Qy    885 CACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAG 944

Db    781 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 840

Qy    945 AAGAAGTGGACCACCTTCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCC 1004

Db    841 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 900

Qy   1005 TTCAACGTCATCCGCCACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATC 1064

Db    901 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 960

Qy   1065 TACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCC 1124
                                               |||||||||||||||||||||||||||| || || ||||||
Db    961 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGCAGGTTGGCGGGACCAGGAGCTCAGCAGTCTGTGCC 1020
```

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Qy   1125 TTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAA 1184
          ||||||||| |||||||||| || ||||||||| ||||| ||||| ||| ||||||| ||
Db   1021 TTCTCTCTCACGGACATTGAGCGAGTCTTTAAAGGGAAGTACAAGGAGCTGAACAAGGAG 1080

Qy   1185 ACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCA 1244
          || || ||||||||| ||||| ||||| | ||| || ||| ||||||||||||||||||
Db   1081 ACCTCCCGCTGGACCACTTACCGGGGCTCAGAGGTCAGCCCGAGGCCAGGCAGTTGCTCC 1140

Qy   1245 GTGGGCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAG 1304
          |||||||||||||| || ||| |||||||||||||||||||||||| |||||||||||||
Db   1141 ATGGGCCCCTCCTCTGACAAAGCCTTGACCTTCATGAAGGACCATTTTCTGATGGATGAG 1200

Qy   1305 CAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTG 1364
          || |||||| || || |||||||||||||||| ||||| ||||||| |||||||||| |||
Db   1201 CACGTGGTAGGAACACCCCTGCTGGTGAAGTCTGGTGTGGAGTACACACGGCTTGCTGTG 1260

Qy   1365 GAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACA 1424
          ||| ||||| | |||||||||||||| |||||||| |||||||||||||| || ||||
Db   1261 GAGTCAGCTCGGGGCCTTGATGGGAGCAGCCATGTGGTCATGTATCTGGGTACCTCCACG 1320

Qy   1425 GGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATT 1484
          ||||| || ||||||||||||| |       | |||||||||||||| |||| ||||| ||||||
Db   1321 GGGTCCCTGCACAAGGCTGTGGTGCCTCAGGACAGCAGTGCTTATCTCGTGGAGGAGATT 1380

Qy   1485 CAGCTGTTCCCTGACCCTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCA 1544
          ||||||    ||||||| |||| ||||||||| |||||||||||||||||   |||||||||||
Db   1381 CAGCTGAGCCCTGACTCTGAGCCTGTTCGAAACCTGCAGCTGGCCCCCGCCCAGGGTGCA 1440

Qy   1545 GTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTAT 1604
          ||||||| ||||||||| ||||| |||||| || ||| | ||||| || |||||||||
Db   1441 GTGTTTGCAGGCTTCTCTGGAGGCATCTGGAGAGTTCCCAGGGCCAATTGCAGTGTCTAC 1500

Qy   1605 GAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCC 1664
          ||||||||||||||||||||| |||||| ||||||| |||||||||||||||||||| ||
Db   1501 GAGAGCTGTGTGGACTGTGTGCTTGCCAGGGACCCTCACTGTGCCTGGGACCCTGAATCA 1560

Qy   1665 CGAACCTGTTGCCTCCTGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGG 1724
          || ||| |||| ||||||| | | | | | ||||||||||||||||| ||
Db   1561 AGACTCTGCAGCCTTCTGTCTGGCTCTACCAACAGGCCTTGGAAGCAGGACATGGAACGC 1620

Qy   1725 GGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGC 1784
          || ||||| |||||||||| ||| || ||||||||||| |||||||| |||| |||||||
Db   1621 GGCAACCCGGAGTGGGTATGCACCCGTGGCCCCATGGCCAGGAGCCCCCGGCGTCAGAGC 1680

Qy   1785 CGCCCGCAAATCATTAAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGC 1844
          | ||| ||| | |||||||||||||||| | |||||||||||||||||||||||| |||||
Db   1681 CCCCCTCAACTAATTAAAGAAGTCCTGACAGTCCCCAACTCCATCCTGGAGCTGCCCTGC 1740

Qy   1845 CCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAA 1904
          ||||||||||||||| || ||||||||| | |||||||||||| ||| | || |||||
Db   1741 CCCCACCTGTCAGCACTGGCCTCTTACCACTGGAGTCATGGCCGAGCCAAAATCTCAGAA 1800

Qy   1905 GCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGT 1964
          ||||||   | |||||||||||||||||||||||||||||| |    |||||||| || |||||
Db   1801 GCCTCTGCTACCGTCTACAATGGCTCCCTCTTGCTGCTGCCGCAGGATGGTGTCGGGGGC 1860

Qy   1965 CTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTG 2024
```

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              |||||||||||    |||  ||||||||| ||||  ||||||||||||| |||||||| |||||
Db      1861  CTCTACCAGTGTGTGGCGACTGAGAACGGCTACTCATACCCTGTGGTCTCCTATTGGGTA  1920

Qy      2025  GACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCAT  2084
              |||||||||||||||| |||||||| ||||| ||||| ||||| ||| | ||||| |||| |
Db      1921  GACAGCCAGGACCAGCCCCTGGCGCTGGACCCTGAGCTGGCGGGCGTTCCCCGTGAGCGT  1980

Qy      2085  GTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTAC  2144
              ||| ||||||||| |||||||||| | || || || || ||||||||||| |||||||
Db      1981  GTGCAGGTCCCGCTGACCAGGGTCGGAGGCGGAGCTTCCATGGCTGCCCAGCGGTCCTAC  2040

Qy      2145  TGGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATC  2204
              |||||||| ||| |||  || || ||||||| | ||| | |||||     |||| ||||
Db      2041  TGGCCCCATTTTCTCATCGTTACCGTCCTCCTGGCCATCGTGCTCCTGGGAGTGCTCACT  2100

Qy      2205  ATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAG  2264
              ||||| | || |||||| || | || || ||||||||||| ||||||||||||||| |
Db      2101  CTCCTCCTCGCTTCCCCACTGGGGGCGCTGCGGGCTCGGGGTAAGGTTCAGGGCTGTGGG  2160

Qy      2265  ACCCTGCGCCC  2275
              |  |||| |||
Db      2161  ATGCTGCCCCC  2171


RESULT 6
BX367242/c
LOCUS        BX367242                1114 bp     mRNA    linear   EST 08-MAY-2003
DEFINITION   BX367242 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
             Homo sapiens cDNA clone CS0DL002YO04 3-PRIME, mRNA sequence.
ACCESSION    BX367242
VERSION      BX367242.1  GI:30455608
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 1114)
  AUTHORS    Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE      Full-length cDNA libraries and normalization
  JOURNAL    Unpublished (2001)
COMMENT      Contact: Genoscope
             Genoscope - Centre National de Sequencage
             BP 191 91006 EVRY cedex - France
             Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
             Library was constructed by Life Technologies, a division of
             Invitrogen. This sequence belongs to sequence cluster 907.f For
             more information about this cluster, see
             http://www.genoscope.cns.fr/
             cgi-bin/cluster.cgi?seq=CS0AL002BH02NP1&cluster=907.f. Contact :
             Feng Liang Email : fliang@lifetech.com URL :
             http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
             Faraday Avenue Genoscope sequence ID : CS0AL002BH02NP1.
FEATURES             Location/Qualifiers
     source          1. .1114
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                     /mol_type="mRNA"
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ORIGIN

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  Query Match          30.2%;  Score 950.6;  DB 13;  Length 1114;
  Best Local Similarity  94.8%;  Pred. No. 1.7e-220;
    Matches  996;  Conservative  24;  Mismatches  27;  Indels   4;  Gaps    4;


Qy    2073 CCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCC 2132
           |||| ||||||||||| ||||||||||||||:|||||||||||| :||||:|||||||||||
Db    1055 CCCCCGGAGCATGT-AAGGTCCCGTTGACMAGGGTCAGTGG-KGGGCSGCCCTGGCTGCC 998


Qy    2133 CAGCAGTCCTACTGGCCCC-ACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTC 2191
           |||:||||::|||| ||||| ||||||| ||||| |||||||||||||||| |||||||||
Db     997 CAGMAGTCMYACTTGCCCCAACTTTGTAACTGTAACTGTCCTCTTTGCCTAAGTGCTTTC 938


Qy    2192 AGGAGCCCTCATCATCCTCGTGGCCTCCCC-ATTGAGAGCACTCCGGGCTCGGGGCAAGG 2250
           |||||||||||||||||||||||||||||| |||||||||:|||||||||||||| ||||||
Db     937 AGGAGCCCTCATCATCCTCGTGGCCTCCCCAATTGAGAGMACTCCGGGCTCGGCGCAAGG 878


Qy    2251 TTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACACC 2310
           ||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     877 TTMAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACACC 818


Qy    2311 TCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACTGCC 2370
           ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db     817 TCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCTAACAACAACTGCC 758


Qy    2371 TAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTGGC 2430
           |||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db     757 TAGGCACTGAGGTMGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTGGC 698


Qy    2431 CATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCAGCACAAAAGACCA 2490
           |||||||||||||||||||||||:|||||||||||||||||:||||||||||||||||||||
Db     697 CATGCTGGCTGGGCGGCCCAAGMACAGCCCTGACTAGGATSACAGCAGCACAAAAGACCA 638


Qy    2491 CCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTG 2550
           |||||||||||||||||||||||||||||||||||||:||||||:|||||||||||||||||
Db     637 CCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATMACTGATVACACTCAGCAGGGTG 578


Qy    2551 ATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAA 2610
           ||| ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db     577 ATGAACAGCAGTCTGCCTCCCCTATGGAACTCCCTTCTACCAAGCACATGAGCTCTCTAA 518


Qy    2611 CAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGAT 2670
           |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db     517 CAGGGTGGGGGCTACCCCCAGACCTGCTCCTAAACTGATATTGAAGAACCTGGAGAGGAT 458


Qy    2671 CCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAGTGTTTCAAGAGACCCTAAA 2730
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       457  CCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAGTGTTTCAAGAGACCCTAAA  398

Qy      2731  AAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTAAACAATCATATGC  2790
              ||||||||:|||||||||||||||||||||||||||||||||||||||||| ||| ||||||
Db       397  AAACCTGCMTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTAAAAAATAATATGC  338

Qy      2791  TAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCT  2850
              |||:||||  ||||||||||||||||:|:||||||||||||||||||| |:|||||| |||||||
Db       337  TAAMATGCAACTCCTGGAAACTCMAMTCTGAAGCTGCCGCTTTGAAMACCAAAACTCCCT  278

Qy      2851  TCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCGCT  2910
              |||||||||||||||:|||||||||||||||||||||||||||||||||:||||||||:|| |||
Db       277  TCTCCCAGGGTCATGMAGGGATCTGCTCCCTCCTGCTTCCCTTACMAGTCGTGMACAGCT  218

Qy      2911  GACTCCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTTCTTCTTGCTTCAGTTGGGGCAG  2970
              ||||||||||||||||| |||||||||||||||||||||| ||| |||| ||||||:| |
Db       217  AACTCCCAGGAAGTCTTCCCTGAAGTCTGACCACCTTTCNTCTAGCTTAAGTTGGRGAAA  158

Qy      2971  ACTCTGATCCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCCTTCTTCACTCCTT  3030
              |||||||||||||||||||||||||||||||||||||||||||||| |||||||||| |||||||
Db       157  ACTCTGATCCCTTCTGCCCTGGCAGAATGGCAGGGGTAATNTGAGCCTTCTTAACTCCTT  98

Qy      3031  TACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTTGTTTTGGGATTCAGAAA  3090
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        97  TACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTTGTTTTGGGATTCAGAAA  38

Qy      3091  ACTGCTTGTCAGAGACTGTTTATTTTTTATT  3121
              ||||||||||||||||||||| ::|||| ||
Db        37  ACTGCTTGTCAGAGACTGTTTCBYTTTTCTT  7
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RESULT 7
BX363741/c
LOCUS   BX363741   1201 bp   mRNA   linear   EST 05-MAY-2003
DEFINITION   BX363741 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
               Homo sapiens cDNA clone CS0DL005YC17 3-PRIME, mRNA sequence.
ACCESSION   BX363741
VERSION   BX363741.1 GI:30384744
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE   Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT   Contact: Genoscope
               Genoscope - Centre National de Sequencage
               BP 191 91006 EVRY cedex - France
               Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
               Library was constructed by Life Technologies, a division of
               Invitrogen. This sequence belongs to sequence cluster 907.f For
               more information about this cluster, see
               http://www.genoscope.cns.fr/
               cgi-bin/cluster.cgi?seq=CS0DL005AB09NP1&cluster=907.f. Contact :
               Feng Liang Email : fliang@lifetech.com URL :

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FEATURES            Location/Qualifiers
     source         1. .1201
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="CS0DL005YC17"
                    /cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
                    /cell_line="RAMOS CELL LINE"
                    /clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
                    25-NORMALIZED"
                    /note="1st strand cDNA was primed with a NotI-oligo(dT)
                    primer. Five prime end enriched, double-strand cDNA was
                    digested with Not I and cloned into the Not I and EcoR V
                    sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
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     Query Match              29.5%;   Score 927.8;   DB 13;   Length 1201;
     Best Local Similarity    95.4%;   Pred. No. 6.6e-215;
     Matches 1001;  Conservative    16;  Mismatches    24;  Indels    8;  Gaps    6;
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Qy     2058 GAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGG 2117
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Db     1042 GATCTGAATGGCAGCATCCCCGGGAGMWGKGARGTCCCGTTGACC-RGGTCAGTGGTGGG 984

Qy     2118 GCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCACTGTCACTGTCCTCTTT 2177
            |  ||  | :||||||||||||||:|:|| |||  ||||||||||||||||||||||||||
Db      983 --CCGCCCTGGYGCCCAGCAGTCCWAYTG--CCCCATTTGTCACTGTCACTGTCCTCTTT 928

Qy     2178 GCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGG 2237
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Db      927 GCCTTAGTGCTTTCA-GAGCCCTCATCATCCTCGT-GCCTCCCCATTGAGAGCACTCCGG 870

Qy     2238 GCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGC 2297
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Db      869 GCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGC 810

Qy     2298 AGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCT 2357
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Db      809 AGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCT 750

Qy     2358 GACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGT 2417
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Db      749 GACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGT 690

Qy     2418 GCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCA 2477
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Db      689 GCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCA 630

Qy     2478 GCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGAC 2537
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Db      629 GCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGAC 570

Qy     2538 ACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCAC 2597
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Qy    2598 ATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGA 2657
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Db     509 ATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGA 450

Qy    2658 ACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAGTGTTTC 2717
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Db     449 ACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAGTGTTTC 390

Qy    2718 AAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTA 2777
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Db     389 AAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTA 330

Qy    2778 AACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGAC 2837
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Db     329 AACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGAC 270

Qy    2838 ACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCA 2897
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Db     269 ACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCA 210

Qy    2898 GTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTTCTTCTTGCT 2957
           |||||||||||||||||:|||||||||||| ||||||:||||||||||||||||||||||
Db     209 GTCGTGCACCGCTGACTYCCAGGAAGTCTTCCCTGAAKTCTGACCACCTTTCTTCTTGCT 150

Qy    2958 TCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG-CAGGGGTAATCTGAGC 3016
           ||||||||||||||:|:||||||||||||||||||||:|||||||| ||||||||||||||
Db     149 TCAGTTGGGGCAGAYTYTGATCCCTTCTGCCCTGGYAGAATGGTCAGGGGTAATCTGAGC 90

Qy    3017 CTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTTGTT 3076
           |||||||||||||||||||||||||||||||||||||||:||||||||:|::|||||||||
Db      89 CTTCTTCACTCCTTTACCCTAGCTGACCCCTTCMCCTCTCCCCBTSSCTTTTCCTTTGTT 30

Qy    3077 TTGGGATTCAGAAAACTGCTTGTCAGAGA 3105
           |||||||||||||||||||||||||||:|
Db      29 TTGGGATTCAGAAAACTGCTTGTCAGAKA 1
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RESULT 8
BX350606/c
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LOCUS       BX350606                922 bp    mRNA    linear   EST 05-MAY-2003
DEFINITION  BX350606 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
            Homo sapiens cDNA clone CS0DL005YC17 3-PRIME, mRNA sequence.
ACCESSION   BX350606
VERSION     BX350606.1  GI:30373499
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 922)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
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FEATURES              Location/Qualifiers
     source           1. .922
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="CS0DL005YC17"
                      /cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
                      /cell_line="RAMOS CELL LINE"
                      /clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
                      25-NORMALIZED"
                      /note="1st strand cDNA was primed with a NotI-oligo(dT)
                      primer. Five prime end enriched, double-strand cDNA was
                      digested with Not I and cloned into the Not I and EcoR V
                      sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
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Query Match   27.8%;   Score 874.4;   DB 13;   Length 922;
Best Local Similarity   98.7%;   Pred. No. 6.3e-202;
Matches 878; Conservative   0; Mismatches   12; Indels   0; Gaps   0;

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Qy      1372 CCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGC 1431
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Db       919 CCCAGGNCCTTGATGGGCACAGCCATCTTGTCATGTACTTGGGAACCACAACAGGGTCGC 860

Qy      1432 TCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGT 1491
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Db       859 TCCACAAGACTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGT 800

Qy      1492 TCCCTGACCCTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTG 1551
             ||||||||||||| |||||||||||||||||||||||| ||||| |||||||||||||
Db       799 TCCCTGACCCTGANCCTGTTCGCAACCTGCAGCTGGCCNCCACCAAGGGTGCAGTGTTGN 740

Qy      1552 TAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCT 1611
             ||||||||||| |||||||||||||||| ||||||||||||||||||||||||||||||||
Db       739 TAGGCTTCTCAGNAGGTGTCTGGAGGGTGCNCCGAGCCAACTGTAGTGTCTATGAGAGCT 680

Qy      1612 GTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCT 1671
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       679 GTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCT 620

Qy      1672 GTTGCCTCCTGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACC 1731
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       619 GTTGCCTCCTGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACC 560

Qy      1732 CAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGC 1791
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       559 CAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGC 500
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Qy    1792 AAATCATTAAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACC 1851
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Db     499 AAATCATTAAAGAAGTCCTGGCTGTCCCTAACTCCATCCTGGAGCTCCCCTGCCCCCACC 440

Qy    1852 TGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTT 1911
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     439 TGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTT 380

Qy    1912 CCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACC 1971
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     379 CCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACC 320

Qy    1972 AGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCC 2031
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     319 AGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCC 260

Qy    2032 AGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGG 2091
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     259 AGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGG 200

Qy    2092 TCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCC 2151
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     199 TCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCC 140

Qy    2152 ACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCG 2211
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     139 ACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCG 80

Qy    2212 TGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGT 2261
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      79 TGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGT 30
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RESULT 9
BX328255

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LOCUS       BX328255                926 bp    mRNA    linear   EST 01-MAY-2003
DEFINITION  BX328255 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
            Homo sapiens cDNA clone CS0DL005YC17 5-PRIME, mRNA sequence.
ACCESSION   BX328255
VERSION     BX328255.1  GI:30307730
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 926)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 907.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0BAG053ZH06_C
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FEATURES   Location/Qualifiers
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                         /organism="Homo sapiens"
                         /mol_type="mRNA"
                         /db_xref="taxon:9606"
                         /clone="CS0DL005YC17"
                         /cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
                         /cell_line="RAMOS CELL LINE"
                         /clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
                         25-NORMALIZED"
                         /note="1st strand cDNA was primed with a NotI-oligo(dT)
                         primer. Five prime end enriched, double-strand cDNA was
                         digested with Not I and cloned into the Not I and EcoR V
                         sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match   27.3%; Score 856.6; DB 13; Length 926;
  Best Local Similarity   98.1%; Pred. No. 1.4e-197;
  Matches 909; Conservative   0; Mismatches   14; Indels   4; Gaps   4;

Qy   805 TGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGG-AGACAGCCAGCGAG 863
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db   1 TGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAAGACAGCCAGCGAG 60

Qy   864 TTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTG 923
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTG 120

Qy   924 GGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCCAGCTGCTCTGC 983
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCCAGCTGCTCTGC 180

Qy   984 ACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCCTGCTCCCCGCCGAT 1043
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCCTGCTCCCCGCCGAT 240

Qy   1044 TCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACC 1103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACC 300

Qy   1104 AGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAA 1163
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAA 360

Qy   1164 TACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAAC 1223
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Db   361 TACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAAC 420

Qy   1224 CCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAG 1283
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAG 480

Qy   1284 GACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTG 1343

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Db     481   GACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTG  540

Qy    1344   GAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTC  1403
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Db     541   GAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTC  600

Qy    1404   ATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGT  1463
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601   ATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGT  660

Qy    1464   GCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACCCTGAACCTGTTCGCAACCTGCAG  1523
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Db     661   GCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACCCTGAACCTGTTCGCAACCTGCAG  720

Qy    1524   CTGGCCCCCACCCAGGGTGCA-GTGTTTGTAGGCTTCTCAGGAGGTGTCTGG-AGGGTGC  1581
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Db     721   CTGGCCCCCACCCCAGGTGCANGTGTTTGTAGGCTTCTCAGGAGGTGTCTGGNAGGGTGC  780

Qy    1582   CCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCC  1641
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Db     781   CCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCCGGACCCCC  840

Qy    1642   ACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCCAACCTGAACT  1701
                  |||||||||||||||||||||||||  |||||||||  |||||||||||||||    |||
Db     841   -CTGTGCCTGGGACCCTGAGTCCCGACCCTGTTGCCTTCTGTCTGCCCCCAACCTTGACT  899

Qy    1702   CCTGGAAGCAGGACATGGAGCGGGGGA  1728
                  |||  |  |    ||||||||||||| |
Db     900   CCTTGGAAGCAGACATGGAGCGGGGAA  926
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RESULT 10
BX384966
LOCUS   BX384966   1201 bp   mRNA   linear   EST 08-MAY-2003
DEFINITION BX384966 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
            Homo sapiens cDNA clone CS0DL005YC17 5-PRIME, mRNA sequence.
ACCESSION   BX384966
VERSION   BX384966.1 GI:30436505
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE   Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT   Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 907.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DL005AB09QP1&cluster=907.f. Contact :

FEATURES   Location/Qualifiers
    source   1. .1201
                            /organism="Homo sapiens"
                            /mol_type="mRNA"
                            /db_xref="taxon:9606"
                            /clone="CS0DL005YC17"
                            /cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
                            /cell_line="RAMOS CELL LINE"
                            /clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
                            25-NORMALIZED"
                            /note="1st strand cDNA was primed with a NotI-oligo(dT)
                            primer. Five prime end enriched, double-strand cDNA was
                            digested with Not I and cloned into the Not I and EcoR V
                            sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match   27.0%;   Score 849.2;   DB 13;   Length 1201;
  Best Local Similarity   97.0%;   Pred. No. 1e-195;
  Matches 871; Conservative   4; Mismatches   22; Indels   1; Gaps   1;

Qy   99 CTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTC 158
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   68 CTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTC 127

Qy   159 TTCCAACTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCC 218
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   128 TTCCAACTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCC 187

Qy   219 ATGCCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAG 278
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   188 ATGCCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAG 247

Qy   279 AAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTG 338
             |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db   248 AAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGCTGATGGAAATACTCTCTACGTG 307

Qy   339 GGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAG 398
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   308 GGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAG 367

Qy   399 AACATGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAG 458
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   368 AACATGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAG 427

Qy   459 AGCAATGAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCAT 518
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   428 AGCAATGAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCAT 487

Qy   519 CTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGAT 578
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   488 CTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGAT 547

Qy   579 TCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTT 638
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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Db       548  TCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTT  607

Qy       639  GACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATG  698
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       608  GACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATG  667

Qy       699  AACAACTTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTC  758
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       668  AACAACTTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTC  727

Qy       759  AAGACCGACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCT  818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       728  AAGACCGACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCT  787

Qy       819  TCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAG  878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       788  TCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAG  847

Qy       879  AGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTG  938
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||:|||
Db       848  AGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCG-AAARCTG  906

Qy       939  CTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGC  996
              |||||||||||||||||||:|||  |     |    |  |  ||:    :     ||| | |    ||
Db       907  CTGCAGAAGAAGTGGACCMCCTCCTGAAGCCCACYGCYCTCMCCAGCCCGGGCACTGC  964


RESULT 11
BQ057192
LOCUS       BQ057192                974 bp    mRNA    linear   EST 29-MAR-2002
DEFINITION  AGENCOURT_6769628 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5812383
            5', mRNA sequence.
ACCESSION   BQ057192
VERSION     BQ057192.1  GI:19816532
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 974)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lou Staudt
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2062  row: 1  column: 16
            High quality sequence stop: 714.
FEATURES             Location/Qualifiers
     source          1. .974
                     /organism="Homo sapiens"
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                         /mol_type="mRNA"
                         /db_xref="taxon:9606"
                         /clone="IMAGE:5812383"
                         /tissue_type="lymphoma, cell line"
                         /lab_host="DH10B (phage-resistant)"
                         /clone_lib="NIH_MGC_99"
                         /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
                         EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                         into EcoRI/XhoI sites using the following 5' adaptor:
                         GGCACGAG(G). Size-selected >500bp for average insert size
                         1.8kb. Library constructed by Ling Hong in the laboratory
                         of Gerald M. Rubin (University of California, Berkeley)
                         using ZAP-cDNA synthesis kit (Stratagene) and Superscript
                         II RT (Life Technologies). Note: this is a NIH_MGC
                         Library."
          ORIGIN

             Query Match              26.3%;  Score 827.4;  DB 13;  Length 974;
             Best Local Similarity  92.6%;  Pred. No. 1.9e-190;
             Matches  902; Conservative    0; Mismatches   67; Indels    5; Gaps    3;

    Qy         92 TCTGTGGCTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCT 151
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    Db          1 TCTGTGGCTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCT 60

    Qy        152 TTTCCTCTTCCAACTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGGAGGCGGGCA 211
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    Db         61 TTTCCTCTTCCAACTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGGAGGCGGGCA 120

    Qy        212 GGGGCCCATGCCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTT 271
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    Db        121 GGGGCCCATGCCCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTT 180

    Qy        272 CCACCAGAAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCT 331
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    Db        181 CCACCAGAAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCT 240

    Qy        332 CTACGTGGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAG 391
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    Db        241 CTACGTGGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAG 300

    Qy        392 GCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAA 451
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    Db        301 GCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAA 360

    Qy        452 GAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGT 511
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    Db        361 GAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGT 420

    Qy        512 CACCCATCTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACT 571
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    Db        421 CACCCATCTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACT 480

    Qy        572 TCAAGATTCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAG 631
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    Db        481 TCAAGATTCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAG 540
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Qy      632 CCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGG 691
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 CCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGG 600

Qy      692 TACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCC 751
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 TACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCC 660

Qy      752 TGTCCTCAAGACCGACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGC 811
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 TGTCCTCAAGACCGACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGC 720

Qy      812 CATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTT 871
            |||||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||
Db      721 CATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGGAGAGACAGCCAGCGAGTTTGACTT 780

Qy      872 CTTTGAGAGGCTCCACACATCGCGGGTGG-CTAGAGTCTGCAAGAATGACGTGGGC-GGC 929
            ||||||||||| ||    |  ||  ||||  ||  |||  |||||||| |  ||||||||||| |||
Db      781 CTTTGAGAGGCCCCCACCCTCCCGGGGGGCCTANAGTCTGCCAAAATGACGTGGGCGGGC 840

Qy      930 GAAAAGCTGCTGCAGAAGAA---GTGGACCACCTTCCTGAAGGCCCAGCTGCTCTGCACC 986
            |||||||||||||| ||  ||    |     || | | |  |||||||||||||||||||||  ||
Db      841 GAAAAGCTGCTGCAAAAAAAAGTGGACCCCCCTTCCTTGAAGGCCCAGCTGCTCTGGCCC 900

Qy      987 CAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCCTGCTCCCCGCCGATTCT 1046
            |   | |||  |     |       |    | ||   | |||   |  | |||  ||       |
Db      901 CCAGCCGGGGGGGAGCTTGCCCTTTCACGTCATTCCCGCCCCCGGGGTCCTGGCTCCCCCC 960

Qy     1047 CCCACAGCTCCCCA 1060
            || |    ||||||
Db      961 CCGAATTTTCCCCA 974
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RESULT 12
BX390196
LOCUS   BX390196   960 bp   mRNA   linear   EST 08-MAY-2003
DEFINITION BX390196 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
            cDNA clone CS0DD003YE08 5-PRIME, mRNA sequence.
ACCESSION   BX390196
VERSION   BX390196.1 GI:30463276
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 960)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE   Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT   Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 907.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/

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FEATURES                  Location/Qualifiers
     source               1. .960
                          /organism="Homo sapiens"
                          /mol_type="mRNA"
                          /db_xref="taxon:9606"
                          /clone="CS0DD003YE08"
                          /tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"
                          /clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
                          /note="1st strand cDNA was primed with a NotI-oligo(dT)
                          primer. Five prime end enriched, double-strand cDNA was
                          digested with Not I and cloned into the Not I and EcoR V
                          sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
```

```
   Query Match              26.2%;   Score 822.2;  DB 13;  Length 960;
   Best Local Similarity    97.2%;   Pred. No. 3.6e-189;
   Matches  900; Conservative    0;  Mismatches   19;  Indels    7;  Gaps    6;


Qy     1530 CCCACCCAGGGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCC 1589
            |||  |||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db       10 CCCCACCAGGGTGCAGTGTTTGTAGGCTTCT-AGGAGGTGTCTGGAGGGTGCCCCGAGCC 68


Qy     1590 AACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCC 1649
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       69 AACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCC 128


Qy     1650 TGGGACCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCCAACCTGAACTCCTGGAAG 1709
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      129 TGGGACCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCCAACCTGAACTCCTGGAAG 188


Qy     1710 CAGGACATGGAGCGGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGC 1769
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      189 CAGGACATGGAGCGGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGC 248


Qy     1770 CTTCGGCCTCAGAGCCGCCCGCAAATCATTAAAGAAGTCCTGGCTGTCCCCAACTCCATC 1829
            ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db      249 CTTCGGCCTCAGAGCCGCCCGCAAATCATTAAAGAAGTCCTGGCTGTCCCTAACTCCATC 308


Qy     1830 CTGGAGCTCCCCTGCCCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCA 1889
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      309 CTGGAGCTCCCCTGCCCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCA 368


Qy     1890 GCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAG 1949
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      369 GCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAG 428


Qy     1950 GATGGAGTTGGGGGTCTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTG 2009
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      429 GATGGAGTTGGGGGTCTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTG 488


Qy     2010 ATCTCCTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGC 2069
            ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      489 ATCTCCTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGC 548
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Qy    2070 ATCCCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCT 2129
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     549 ATCCCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCT 608

Qy    2130 GCCCAGCAGTCCTACTGGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTT 2189
           ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db     609 GCCCAGCAGTCCTACTGGCCCCACTNTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTT 668

Qy    2190 TCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAG 2249
           ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db     669 TCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTTCGGGCAAG 728

Qy    2250 GTTC-AGGGCTGTGAGACCCTGCGCCCTGGGG--AGAAGGCCCCGTTAAGCAGAGAGCAA 2306
           |||| ||||||||||||||||||||||||||||    | ||||||||||||||||||||||
Db     729 GTTCAAGGGCTGTGAGACCCTGCGCCCTGGGGGAGAAGGGCCCCGTTAAGCAGAGAGCAA 788

Qy    2307 CA-CCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACG-CTGACAACA 2364
           || ||| |||||||||||||||||||||||||||||||||||||||||| || ||||||||
Db     789 CACCCTTCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGGCGCCTGACAACA 848

Qy    2365 ACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCA 2424
           |||||||||||||||||||||||||||||||||| ||||||  |||||   |||||  |||| ||
Db     849 ACTGCCTAGGCACTGAGGTAGCTTAAACTCTA-GCACAGCCCGGGCTTGCGGGGCAGCCA 907

Qy    2425 CCTGGCCATGCTGGCTGGGCGGCCCA 2450
           |||| |||||||||  ||||||||||||
Db     908 CCTGCCCATGCTGTGTGGGCGGCCCA 933


RESULT 13
CB243787/c
LOCUS       CB243787                 797 bp    mRNA    linear    EST 12-FEB-2003
DEFINITION  UI-CF-FN0-agg-a-05-0-UI.s1 UI-CF-FN0 Homo sapiens cDNA clone
            UI-CF-FN0-agg-a-05-0-UI 3', mRNA sequence.
ACCESSION   CB243787
VERSION     CB243787.1  GI:28365431
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 797)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: McCray, PB
            McCray Lab
            University of Iowa
            2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
            Tel: 319 356 4866
            Fax: 319 356 7171
            Email: paul-mccray@uiowa.edu
            Tissue Procurement: Dr. M. J. Welsh, University of Iowa
```

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
The following repetitive elements were found in this cDNA
sequence: 1-46, >AT_rich#Low_complexity (matched compliment)
Seq primer: M13 FORWARD
POLYA=Yes.

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FEATURES              Location/Qualifiers
      source          1. .797
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                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="UI-CF-FN0-agg-a-05-0-UI"
                      /tissue_type="Human Lung Epithelial cells"
                      /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                      /clone_lib="UI-CF-FN0"
                      /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                      modified polylinker; Site_1: EcoR I; Site_2: Not I;
                      UI-CF-FN0 is a subtracted cDNA library derived from two
                      normalized Human lung epithelial cell libraries (EN1 and
                      DU1) The library was subtracted according to according to
                      Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                      1996. For additional information, contact:
                      bento-soares@uiowa.edu
                      TAG_TISSUE=Human Lung Epithelial Cell Lines untreated LPS
                      6hr to LPS 24h
                      TAG_LIB=UI-CF-FN0
                      TAG_SEQ=CTGCTCAGGT"
ORIGIN
```

Query Match   24.8%;   Score 779.8;   DB 14;   Length 797;
Best Local Similarity   99.4%;   Pred. No. 7.3e-179;
Matches 781; Conservative   0; Mismatches   5; Indels   0; Gaps   0;

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Qy     2358 GACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGT 2417
            |||||||||||| ||||||||||||||||||||||||| |||||||||||||||||||||
Db      797 GACAACAACTGCNTAGGCACTGAGGTAGCTTAAACTNTAGGCACAGGCCGGGGCTGCGGT 738

Qy     2418 GCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCA 2477
            ||||||||| |||||||||||||||||||||||||||||||||||| ||||||||||||
Db      737 GCAGGCACCCGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGANTAGGATGACAGCA 678

Qy     2478 GCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGAC 2537
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      677 GCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGAC 618

Qy     2538 ACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCAC 2597
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Db      617 ACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCAC 558

Qy     2598 ATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGA 2657
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      557 ATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGA 498
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Qy    2658 ACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAGTGTTTC 2717
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     497 ACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAGTGTTTC 438

Qy    2718 AAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTA 2777
           |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db     437 AAGAGACCCTAAAAAACCTGCCTGTCCTAGGACCCTATGGTAATGAACACCAAACATCTA 378

Qy    2778 AACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGAC 2837
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     377 AACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGAC 318

Qy    2838 ACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCA 2897
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     317 ACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCA 258

Qy    2898 GTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTTCTTCTTGCT 2957
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     257 GTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGACCACCTTTCTTCTTGCT 198

Qy    2958 TCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCC 3017
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Db     197 TCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCC 138

Qy    3018 TTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTTGTTT 3077
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     137 TTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTTGTTT 78

Qy    3078 TGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTATTAAAAATATAAGGCTTA 3137
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      77 TGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTATTAAAAATATAAGGCTTA 18

Qy    3138 AAAAAA 3143
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Db      17 AAAAAA 12
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RESULT 14
BX112994

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LOCUS          BX112994                  801 bp    mRNA     linear   EST 07-FEB-2003
DEFINITION     BX112994 Soares placenta Nb2HP Homo sapiens cDNA clone
               IMAGp998F02225 ; IMAGE:147841, mRNA sequence.
ACCESSION      BX112994
VERSION        BX112994.1  GI:27837970
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
  ORGANISM     Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1  (bases 1 to 801)
  AUTHORS      Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
               Radelof,U., Schneider,D. and Korn,B.
  TITLE        Human UnigeneSet - RZPD3
  JOURNAL      Unpublished (2003)
  COMMENT      Contact: Ina Rolfs
               RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
               Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
```

RZPD; IMAGp998F02225.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-
bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.

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FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGp998F02225 ; IMAGE:147841"
                     /sex="Female"
                     /dev_stage="placenta obtained at birth (full term)"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares placenta Nb2HP"
                     /note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     AACTGGAAGAATTCGCGGCCGCAGGAATTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo.   "
ORIGIN
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   Query Match            24.7%;  Score 775;  DB 13;  Length 801;
   Best Local Similarity   99.4%;  Pred. No. 1.1e-177;
   Matches  797; Conservative   0; Mismatches   3; Indels  2; Gaps  2;

Qy    2086 TGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACT 2145
           |||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db       1 TGAAGGTCCCGTTGACC-GGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACT 59

Qy    2146 GGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCA 2205
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      60 GGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCA 119

Qy    2206 TCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGA 2265
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     120 TCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGA 179

Qy    2266 CCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGG 2325
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     180 CCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGG 239

Qy    2326 AATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAG 2385
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     240 AATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAG 299
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Qy    2386 CTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCG 2445
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Db     300 CTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCG 359

Qy    2446 GCCCAAGCACAGCCCTGACTAGGATGACAGCAGCACAAAGACCACCTTTCTCCCCTGAG 2505
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     360 GCCCAAGCACAGCCCTGACTAGGATGACAGCAGCACAAAGACCACCTTTCTCCCCTGAG 419

Qy    2506 AGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTG 2565
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Db     420 AGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTG 479

Qy    2566 CCTCCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTAC 2625
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Db     480 CCTCCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTAC 539

Qy    2626 CCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCC 2685
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     540 CCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCC 599

Qy    2686 ATTCCAGGGACCCTCCAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCC 2745
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Db     600 ATTCCAGGGACCCTCCAGAAACACAGTGNTTCAAGAGACCCTAAAAAACCTGCCTGTCCC 659

Qy    2746 AGGACCCTATGGTAATGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCT 2805
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Db     660 AGGACCCTATGGTAATGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCT 719

Qy    2806 GGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATG 2865
           |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
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Qy    2866 CA-GGGATCTGCTCCCTCCTGC 2886
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RESULT 15
BQ883972

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LOCUS        BQ883972                 912 bp    mRNA    linear   EST 16-AUG-2002
DEFINITION   AGENCOURT_8616305 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6302388
             5', mRNA sequence.
ACCESSION    BQ883972
VERSION      BQ883972.1  GI:22275980
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1  (bases 1 to 912)
  AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
  TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL    Unpublished (1999)
  COMMENT    Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Dr. Mark Watson
```

```
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2519  row: m  column: 13
            High quality sequence stop: 601.
FEATURES                 Location/Qualifiers
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                         /mol_type="mRNA"
                         /db_xref="taxon:9606"
                         /clone="IMAGE:6302388"
                         /lab_host="DH10B (phage-resistant)"
                         /clone_lib="NIH_MGC_113"
                         /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                         EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                         into EcoRI/XhoI sites using the following 5' adaptor:
                         GGCACGAG(G). Library constructed  by Ling Hong in the
                         laboratory of Gerald M. Rubin (University of  California,
                         Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                         Superscript II RT (Life Technologies). Note: this is a
                         NIH_MGC Library."
      ORIGIN

     Query Match          24.5%;  Score 769.8;  DB 13;  Length 912;
     Best Local Similarity  96.7%;  Pred. No. 2.2e-176;
     Matches  840;  Conservative   0;  Mismatches  22;  Indels   7;  Gaps   5;
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Qy      1315 GGACGCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCC 1374
             ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db         1 GGACGCCCCTGCTGGTGAAATCTGGCGTGGAG-ATACACGGCTTGCAGTGGAGACAGCCC 59

Qy      1375 AGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCC 1434
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        60 AGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCC 119

Qy      1435 ACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCC 1494
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       120 ACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCC 179

Qy      1495 CTGACCCTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAG 1554
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       180 CTGACCCTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAG 239

Qy      1555 GCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTG 1614
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Db       240 GCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTG 299

Qy      1615 TGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTT 1674
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Db       300 TGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTT 359

Qy      1675 GCCTCCTGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAG 1734
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Qy   1735 AGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAA 1794
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    420 AGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAA 479

Qy   1795 TCATTAAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGT 1854
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Db    480 TCATTAAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGT 539

Qy   1855 CAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCA 1914
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    540 CAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCA 599

Qy   1915 CTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGT 1974
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    600 CTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGT 659

Qy   1975 GCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGG 2034
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    660 GCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGG 719

Qy   2035 ACCAGACCCT-GGCCCTGGATCCTGAACTGGCAGGCAT-CCCCCGGGAGCATGTGAAGGT 2092
          | ||||||||| ||||||||||||||||||||| |||||| |||||||||||||||||| ||
Db    720 AACAGACCCTGGGCCCTGGATCCTGAACTGGGAGGCATCCCCCCGGGAGCATGTGAAAGT 779

Qy   2093 CCCGTTGACCAGGGTCAGTGG--TGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCC 2150
          ||||||||||||||| ||| ||| | ||| | |||||| || ||||||||||
Db    780 CCCGTTGACCAGGGTCCATGGGTGGGGCCGGCCTGGCTTGCCCAACAATCCTACTGGCCC 839

Qy   2151 C--ACTTTGTCACTGTCACTGTCCTCTTT 2177
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Db    840 CCACTTTGGCCACTGTTACTGGCCCCCTT 868
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Search completed: May 13, 2004, 15:34:10
Job time : 7730 secs

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                          GenCore version 5.1.6
                  Copyright (c) 1993 - 2004  Compugen Ltd.


OM nucleic - nucleic search, using sw model

Run on:           May 13, 2004, 07:58:58 ; Search time 12062 Seconds
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Title:            US-10-015-391A-276
Perfect score:    3143
Sequence:         1 gggctgaggcactgagagac..........aaatataaggcttaaaaaaa 3143


Scoring table:    IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0


Searched:         3470272 seqs, 21671516995 residues


Total number of hits satisfying chosen parameters:      6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries


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40:  em_htgo_mus:*
41:  em_htgo_other:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

<div align="center">SUMMARIES</div>

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	3	3068.4	97.6	3257	9	BC020974	BC020974 Homo sapi
	4	3041.4	96.8	3252	9	AB029394	AB029394 Homo sapi
	5	3035.8	96.6	3191	6	BD249136	BD249136 27 human
	6	2927.6	93.1	3151	9	HSM807023	BX640891 Homo sapi
	7	2682.2	85.3	2981	6	AX746794	AX746794 Sequence
	8	2682.2	85.3	2981	9	AK091127	AK091127 Homo sapi
	9	2476.4	78.8	2768	6	AX512887	AX512887 Sequence
c	10	2281	72.6	2281	6	AX528271	AX528271 Sequence
	11	2228.4	70.9	2271	6	AX528269	AX528269 Sequence
	12	1834.8	58.4	1838	6	AX879068	AX879068 Sequence
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	15	1760	56.0	3159	10	BC025800	BC025800 Mus muscu
	16	1727.6	55.0	3046	10	MMRNASEMB	X85991 M.musculus
	17	1340	42.6	164168	9	AL135927	AL135927 Human DNA
c	18	1340	42.6	164179	9	AC007227	AC007227 Homo sapi
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c	21	498	15.8	567	6	AX872305	AX872305 Sequence
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	23	494	15.7	1223	6	AX704742	AX704742 Sequence
	24	486.6	15.5	184850	2	AC102388	AC102388 Mus muscu
	25	486.6	15.5	249206	2	AC145168	AC145168 Mus muscu
	26	470	15.0	988	6	AX430331	AX430331 Sequence
	27	439.6	14.0	230635	2	AC128319	AC128319 Rattus no
	28	439.6	14.0	246036	2	AC097816	AC097816 Rattus no
	29	439.6	14.0	289877	2	AC119762	AC119762 Rattus no
	30	327	10.4	2405	6	AX879101	AX879101 Sequence
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	33	280.4	8.9	106784	2	AC136250	AC136250 Rattus no

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34    263.6    8.4    3766    6    BD171175            BD171175 Novel gen
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37    263.6    8.4    3781    6    AX376386            AX376386 Sequence
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39    263.6    8.4    3781    9    AY358392            AY358392 Homo sapi
40    263.6    8.4    3807    9    AY445887            AY445887 Homo sapi
41    251.6    8.0    3528    9    AK026108            AK026108 Homo sapi
42    246.6    7.8    2390    6    AX418422            AX418422 Sequence
43    237.8    7.6    3293    6    AX174731            AX174731 Sequence
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RESULT 1
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LOCUS          AX697208                3143 bp    DNA        linear    PAT 02-APR-2003
DEFINITION     Sequence 276 from Patent WO0078961.
ACCESSION      AX697208
VERSION        AX697208.1  GI:29498147
KEYWORDS       .
SOURCE         Homo sapiens (human)
  ORGANISM     Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
  AUTHORS      Ferrara,N., Stewart,T.A., Williams,P.M., Baker,K.P., Desnoyers,L.,
               Eaton,D.L., Gao,W.Q., Pan,J., Botstein,D., Fong,S., Goddard,A.,
               Godowski,P.J., Gurney,A.L., Smith,V., Tumas,D., Wood,W.I.,
               Grimaldi,C.J., Hillan,K.J., Paoni,N.F., Roy,M.A. and Watanabe,C.K.
  TITLE        Secreted and transmembrane polypeptides and nucleic acids encoding
               the same
  JOURNAL      Patent: WO 0078961-A 276 28-DEC-2000;
               Genentech Inc. (US)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match           100.0%;  Score 3143;  DB 6;  Length 3143;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 3143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60
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Qy       61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120
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Qy      121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180
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Db    121  TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC  180

Qy    181  TGCCGACGACGACCGCGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG  240
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Db    181  TGCCGACGACGACCGCGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG  240

Qy    241  CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA  300
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Db    241  CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA  300

Qy    301  CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG  360
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    301  CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG  360

Qy    361  CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA  420
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Qy    481  ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG  540
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Qy    541  CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG  600
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Db    541  CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG  600

Qy    601  AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG  660
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Qy    661  CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC  720
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Db    661  CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC  720

Qy    721  CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT  780
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Db    721  CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT  780

Qy    781  GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT  840
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Db    781  GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT  840

Qy    841  TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  900
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Db    841  TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  900

Qy    901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960
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Db    901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960

Qy    961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020
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           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1081  CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA  1140
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Qy   1201  CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG  1260
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Qy   1321  CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC  1380
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Qy   1381  TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG  1440
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Qy   1441  CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC  1500
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Qy   1501  CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT  1560
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Qy   1561  CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT  1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561  CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT  1620

Qy   1621  GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC  1680
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Qy   1681  TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG  1740
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Qy   1741  CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA  1800
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Db   1741  CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA  1800

Qy   1801  AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT  1860
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Qy    1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920
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Qy    2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460
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Qy     2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760
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RESULT 2
AY358531
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DEFINITION Homo sapiens clone DNA71166 semaphorin B (UNQ783) mRNA, complete
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ACCESSION   AY358531
VERSION   AY358531.1 GI:37182184
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SOURCE   Homo sapiens (human)
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 3143)
  AUTHORS   Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
            Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
            Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
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            Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
            Goddard,A., Wood,W.I. and Godowski,P.
  TITLE   The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
            Effort to Identify Novel Human Secreted and Transmembrane Proteins:

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ORIGIN

     Query Match   100.0%; Score 3143; DB 9; Length 3143;
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RESULT 3
BC020974
LOCUS            BC020974                3257 bp    mRNA    linear    PRI 03-OCT-2003
DEFINITION       Homo sapiens hypothetical protein FLJ12287 similar to semaphorins,
                 mRNA (cDNA clone MGC:9542 IMAGE:3847802), complete cds.
ACCESSION        BC020974
VERSION          BC020974.1  GI:18088092
KEYWORDS         MGC.
SOURCE           Homo sapiens (human)
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                 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE        1  (bases 1 to 3257)
  AUTHORS        Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
                 Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
                 Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
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                 Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
                 Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
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                 Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
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                 Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
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                 Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
                 Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE   Generation and initial analysis of more than 15,000 full-length
                 human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932
REFERENCE   2   (bases 1 to 3257)
  AUTHORS   Strausberg,R.
  TITLE   Direct Submission
  JOURNAL   Submitted (03-JAN-2002) National Institutes of Health, Mammalian
                 Gene Collection (MGC), Cancer Genomics Office, National Cancer
                 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                 USA
  REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT   Contact: MGC help desk
                 Email: cgapbs-r@mail.nih.gov
                 Tissue Procurement: ATCC
                 cDNA Library Preparation: Life Technologies, Inc.
                 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                 DNA Sequencing by: Sequencing Group at the Stanford Human Genome
                 Center, Stanford University School of Medicine, Stanford, CA   94305
                 Web site: http://www-shgc.stanford.edu
                 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
                 Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                 R. M.

                 Clone distribution: MGC clone distribution information can be found
                 through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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ORIGIN

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Qy   1274  CTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCCTGCTGGTGAA  1333
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Db   1367  CTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCCTGCTGGTGAA  1426

Qy   1334  ATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCCTTGATGGGCACAG  1393
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Qy   1394 CCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGG 1453
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Db   1487 CCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGG 1546

Qy   1454 GGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACCCTGAACCTGTTCG 1513
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Qy   1514 CAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGTCTG 1573
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Qy   1574 GAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCG 1633
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Qy   1634 GGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCCAA 1693
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RESULT 4
AB029394

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DEFINITION  Homo sapiens mRNA for SEMB, complete cds.
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VERSION     AB029394.1  GI:12248381
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SOURCE      Homo sapiens (human)
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  AUTHORS   Seki,N., Hattori,A., Hayashi,A., Kozuma,S., Muramatsu,M.,
            Miyajima,N. and Saito,T.
  TITLE     Human semaphorin B
  JOURNAL   Published Only in DataBase (2001)
REFERENCE   2  (bases 1 to 3252)
  AUTHORS   Seki,N., Hattori,A., Hayashi,A., Kozuma,S., Muramatsu,M.,
            Miyajima,N. and Saito,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-JUN-1999) Toshiyuki Saito, National Institute of
            Radiological Sciences, Genome Research Group; Inage-ku Anagawa
            4-9-1, Chiba, Chiba 263-8555, Japan (E-mail:t_saito@nirs.go.jp,
            Tel:81-43-201-3135, Fax:81-43-251-9818)
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KECRTSASDVDADNNCLGTEVA"

ORIGIN

Query Match   96.8%; Score 3041.4; DB 9; Length 3252;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 3074; Conservative   0; Mismatches   16; Indels   3; Gaps   2;

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Qy   2265 ACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAG 2324
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Qy   2325 GAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTA 2384
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Db   2492 GCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGC 2551

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Qy    2505 GAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCT 2564
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Db    2612 GAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCT 2671

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RESULT 5
BD249136
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DEFINITION 27 human secreted proteins.
ACCESSION   BD249136
VERSION   BD249136.1 GI:33058906
KEYWORDS   JP 2002538841-A/10.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 3191)

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AUTHORS    Ruben,S.M., Ni,J., Ebner,R., Rosen,C.A., Shi,Y., Birse,C.,
           Florence,K., Komatsoulis,G., Lafleur,D.W., Moore,P.A., Olsen,H.S.
           and Young,P.E.
TITLE      27 human secreted proteins
JOURNAL    Patent: JP 2002538841-A 10 19-NOV-2002;
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           PD   19-NOV-2002
           PF   16-MAR-2000 JP 2000605787
           PR   18-MAR-1999 US   60/125055
           PI   STEVEN M RUBEN,JIAN NI,REINHARD EBNER,CRAIG
           A ROSEN,YANGGU SHI,
           PI   CHARLES BIRSE,KIMBERLY FLORENCE,GEORGE KOMATSOULIS,DAVID W  PI
             LAFLEUR,
           PI   PAUL A MOORE,HENRIK S OLSEN,PAUL E YOUNG
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ORIGIN

   Query Match            96.6%;  Score 3035.8;  DB 6;  Length 3191;
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Qy     103 GCATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCC 162
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Db      78 GCATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCC 137

Qy     163 AACTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGGAGGCGGGCAGGGGCCCATGC 222
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Db     138 AACTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGGAGGCGGGCAGGGGCCCATGC 197

Qy     223 CCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGG 282
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Db      198 CCAGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGG 257

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Db      258 GCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGG 317

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Db      318 CTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACA 377

Qy      403 TGATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCA 462
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Db      498 ACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCT 557

Qy      583 ACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACC 642
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Db      558 ACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACC 617

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Db      618 CCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACA 677

Qy      703 ACTTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGA 762
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Db      738 CCGACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGA 797

Qy      823 CCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGC 882
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Db      798 CCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGC 857

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Db      858 TCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGC 917

Qy      943 AGAAGAAGTGGACCACCTTCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGC 1002
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Db      918 AGAAGAAGTGGACCACCTTCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGC 977

Qy      1003 CCTTCAACGTCATCCGCCACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACA 1062
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      978 CCTTCAACGTCATCCGCCACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACA 1037

Qy      1063 TCTACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTG 1122
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Qy   1123 CCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAG 1182
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Qy   1303 AGCAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAG 1362
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Db   1278 AGCAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAG 1337

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Qy   1423 CAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGA 1482
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Qy   1963 GTCTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGG 2022
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Qy   2023 TGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGC 2082
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Db   2298 AGGAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGG 2357

Qy   2383 TAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGG 2442
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RESULT 6
HSM807023

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LOCUS       HSM807023               3151 bp    mRNA     linear   PRI 28-AUG-2003
DEFINITION  Homo sapiens mRNA; cDNA DKFZp686D04248 (from clone DKFZp686D04248);
            complete cds.
ACCESSION   BX640891
VERSION     BX640891.1  GI:34365195
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3151)
  AUTHORS   Ottenwaelder,B., Obermaier,B., Deutschenbaur,S., Mewes,H.W.,
            Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.
  CONSRTM   The German Human cDNA Consortium
  TITLE     Direct Submission
  JOURNAL   Submitted (26-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764
            Neuherberg, GERMANY
  COMMENT   Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by MediGenomix (Martinsried/Germany) within the cDNA
            sequencing consortium of the German Genome Project. This clone
            (DKFZp686D04248) is available at the RZPD in Berlin. Please contact
            the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
            information about the clone and the sequencing project is available
            at http://mips.gsf.de/proj/cDNA/.
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ORIGIN
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   Matches 2933; Conservative   0; Mismatches   9; Indels   0; Gaps   0;

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Qy        262 TTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATG 321
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Qy        442 GTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTT 501
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Qy     562  TCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAA  621
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Qy     622  AAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGC  681
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Qy     862  AGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACG  921
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Qy     922  TGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCCAGCTGCTCT  981
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Qy     982  GCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCCTGCTCCCCGCCG  1041
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Qy    1042  ATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGA  1101
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Qy    1102  CCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGA  1161
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Qy    1162  AATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCA  1221
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Db    1160  AATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCA  1219

Qy    1222  ACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTGATAAGGCCCTGACCTTCATGA  1281
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Qy    1282  AGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCG  1341
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Db    1460 GTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACCCTGAACCTGTTCGCAACCTGC 1519

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Qy    2062 TGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCG 2121
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Qy    3142 AA 3143
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Db    3140 AA 3141
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RESULT 7
AX746794

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LOCUS       AX746794                2981 bp    mRNA    linear    PAT 20-JUN-2003
DEFINITION  Sequence 319 from Patent EP1308459.
ACCESSION   AX746794
VERSION     AX746794.1  GI:32131182
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
            Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
            Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
            Masuho,Y.
  TITLE     Full-length cDNA sequences
  JOURNAL   Patent: EP 1308459-A 319 07-MAY-2003;
            Helix Research Institute (JP) ; Research Association for
            Biotechnology (JP)
FEATURES             Location/Qualifiers
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ORIGIN
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  Matches 2793;  Conservative    0;  Mismatches    3;  Indels   99;  Gaps    1;

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Qy     302 TCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGC 361
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Db    412  ------------------------------------------------------------  411


Qy    542  CTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGGA  601
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Db    412  -----------------------GAACTTCAAGATTCCTACCTGTTGCCCATCTCGGA  446


Qy    602  GGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGC  661
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Db    447  GGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGC  506


Qy    662  TGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCC  721
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Db    507  TGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCC  566


Qy    722  CATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCTG  781
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Db    567  CATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCTG  626


Qy    782  GCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTT  841
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    627  GCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTT  686


Qy    842  CTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGC  901
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Db    687  CTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGC  746


Qy    902  TAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTT  961
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Db    747  TAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTT  806


Qy    962  CCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCA  1021
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Qy   1022  CGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCTC  1081
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Db    867  CGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCTC  926


Qy   1082  CCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACAT  1141
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Db    927  CCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACAT  986


Qy   1142  TGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTAC  1201
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Qy   1442 TGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACCC 1501
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Qy   1682 GTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGGC 1741
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Db   1527 GTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGGC 1586

Qy   1742 ATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTAA 1801
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RESULT 8
AK091127

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LOCUS       AK091127                2981 bp    mRNA    linear   PRI 15-JUL-2002
DEFINITION  Homo sapiens cDNA FLJ33808 fis, clone CTONG2001749, highly similar
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ACCESSION   AK091127
VERSION     AK091127.1  GI:21749423
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Nishi,T., Ota,T., Nakagawa,S., Senoh,A., Mizuguchi,H., Inagaki,H.,
            Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
            Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
            Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M.,
            Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K.,
            Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y.,
            Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2981)
  AUTHORS   Isogai,T. and Yamamoto,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7
            Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction: Helix Research Institute (HRI) (supported by Japan
            Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
            HRI, and Biotechnology Center, National Institute of Technology and
            Evaluation; clone selection for full insert sequencing: HRI and
            RAB; annotation: HRI and RAB.
FEATURES             Location/Qualifiers
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                     /clone_lib="CTONG2"
                     /note="cloning vector: pME18SFL3"
ORIGIN
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Query Match              85.3%;   Score 2682.2;   DB 9;   Length 2981;
Best Local Similarity    96.5%;   Pred. No. 0;
Matches 2793;  Conservative     0;  Mismatches     3;   Indels   99;   Gaps     1;

Qy     242 AGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACAC 301
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     186 AGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACAC 245

Qy     302 TCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGC 361
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Qy     422 TGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCAA 481
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Db     366 TGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAG-------------- 411

Qy     482 CTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCGC 541

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Db    2007 TGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCC 2066

Qy    2222 ATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGGA 2281
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Qy    2282 GAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGC 2341
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Qy    2342 CAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCAC 2401
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Db    2187 CAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCAC 2246

Qy    2402 AGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCT 2461
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Db    2247 AGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCT 2306

Qy    2462 GACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACT 2521
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Db    2307 GACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACT 2366

Qy    2522 CTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACT 2581
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Qy    2582 CCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCT 2641
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Db    2427 CCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCT 2486

Qy    2642 ACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCC 2701
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Db    2487 ACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCC 2546

Qy    2702 AGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAAT 2761
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Db     2547 AGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAAT 2606

Qy     2762 GAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGA 2821
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Db     2607 GAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGA 2666

Qy     2822 AGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCT 2881
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Db     2667 AGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCCT 2726

Qy     2882 CCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGAC 2941
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Db     2727 CCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGAC 2786

Qy     2942 CACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGGC 3001
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Db     2787 CACCTTTCTTCTTGCTTCAGTTGGGGCAGACTTTGATCCCTTCTGCCCTGGCAGAATGGC 2846

Qy     3002 AGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCCT 3061
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Db     2847 AGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCCT 2906

Qy     3062 CCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTATT 3121
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Db     2907 CCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTATT 2966

Qy     3122 AAAAATATAAGGCTT 3136
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RESULT 9
AX512887
LOCUS       AX512887                2768 bp    DNA        linear    PAT 03-OCT-2002
DEFINITION  Sequence 35 from Patent WO02062841.
ACCESSION   AX512887
VERSION     AX512887.1  GI:23504046
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Tang,T.Y., Yue,H., Gandhi,A.R., Yao,M.G., Warren,B.A., Ding,L.,
            Duggan,B.M., Xu,Y., Yang,J., Thangavelu,K., Lal,P.G.,
            Honchell,C.D., Walia,N.K., Lee,S., Lee,E.A., Richardson,T.W.,
            Baughn,M.R. and Elliott,V.S.
  TITLE     Secreted proteins
  JOURNAL   Patent: WO 02062841-A 35 15-AUG-2002;
            Incyte Genomics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1..2768
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                     /db_xref="taxon:9606"
                     /note="Incyte ID No: 7487507CB1"
ORIGIN
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Query Match          78.8%;   Score 2476.4;  DB 6;   Length 2768;
Best Local Similarity   96.5%;  Pred. No. 0;
Matches 2580;   Conservative   0;  Mismatches   1;  Indels  93;  Gaps   1;

Qy      74 AGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCC 133
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     169 AGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCC 228

Qy     134 CTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGCTGCCGACGACGAC 193
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     229 CTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGCTGCCGACGACGAC 288

Qy     194 CGCGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATGCAGGGGATGAACG 253
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     289 CGCGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATGCAGGGGATGAACG 348

Qy     254 TAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAG 313
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     349 TAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAG 408

Qy     314 TGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCA 373
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     409 TGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCA 468

Qy     374 GGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAA 433
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     469 GGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAA 528

Qy     434 GAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATCCGTGT 493
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     529 GAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATCCGTGT 588

Qy     494 CCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGC 553
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Db     589 CCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGC 648

Qy     554 TTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGGAGGACAAGGTCAT 613
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Qy     614 GGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGA 673
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Db     709 GGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGA 768

Qy     674 TGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATGCG 733
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Db     769 TGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATGCG 828

Qy     734 CACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCTGGCTGCATCATGA 793
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     829 CACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCTGGCTGCATCATGA 888

Qy     794 CGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGAC 853
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     889 CGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGAC 948
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Qy    854 AGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAA 913
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Db    949 AGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAA 1008

Qy    914 GAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCCA 973
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Db   1009 GAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCCA 1068

Qy    974 GCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCCTGCT 1033
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Db   1069 GCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCCTGCT 1128

Qy   1034 CCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCTCCCAGTGGCAGGT 1093
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Db   1129 CCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCTCCCAGTGGCAGGT 1188

Qy   1094 TGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTT 1153
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Db   1189 TGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTT 1248

Qy   1154 TAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTACTTATAGGGGCCC 1213
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Db   1249 TAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTACTTATAGGGGCCC 1308

Qy   1214 TGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTGATAAGGCCCTGAC 1273
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Db   1309 TGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTGATAAGGCCCTGAC 1368

Qy   1274 CTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCCTGCTGGTGAA 1333
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Db   1369 CTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCCTGCTGGTGAA 1428

Qy   1334 ATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCCTTGATGGGCACAG 1393
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Db   1429 ATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCCTTGATGGGCACAG 1488

Qy   1394 CCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGG 1453
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Db   1489 CCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGCTGT--------- 1539

Qy   1454 GGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACCCTGAACCTGTTCG 1513
Db   1540 ------------------------------------------------------------ 1539

Qy   1514 CAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGTCTG 1573
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Db   1576 GAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCG 1635

Qy   1634 GGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCCAA 1693
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1636 GGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCCAA 1695

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Db   1696 CCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGGCATGTGCCAGTGG 1755

Qy   1754 CCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTAAAGAAGTCCTGGC 1813
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Qy   1874 TTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCT 1933
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Db   1876 TTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCT 1935

Qy   1934 CTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGGCAACTGAGAATGG 1993
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Db   1936 CTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGGCAACTGAGAATGG 1995

Qy   1994 CTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGA 2053
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Db   1996 CTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGA 2055

Qy   2054 TCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGG 2113
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Db   2056 TCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGG 2115

Qy   2114 TGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCACTGTCACTGTCCT 2173
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Qy   2174 CTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACT 2233
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Db   2296 AAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGA 2355

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Db   2356 CGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTG 2415

Qy   2414 CGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGAC 2473
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Qy   2474 AGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGA 2533
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Db     2596 GCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATTG 2655

Qy     2654 AAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAGTG 2713
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Qy     2714 TTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAG 2747
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RESULT 10
AX528271/c
LOCUS       AX528271                2281 bp    DNA        linear    PAT 21-NOV-2002
DEFINITION  Sequence 9 from Patent WO0206339.
ACCESSION   AX528271
VERSION     AX528271.1  GI:25172573
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Spaderna,S.K., Tchernev,V., Liu,X., Shenoy,S., Spytek,K.,
            Zerhusen,B., Patturajan,M., Taupier,R.J., Rastelli,L., Grosse,W.M.,
            Szekeres,E.S., Alsobrook,J.I., Lepley,D.M., Shen,L., Burgess,C.E.,
            Shimkets,R.A. and Padigaru,M.
  TITLE     Proteins and nucleic acids encoding same
  JOURNAL   Patent: WO 0206339-A 9 24-JAN-2002;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
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ORIGIN

   Query Match           72.6%;  Score 2281;  DB 6;  Length 2281;
   Best Local Similarity  100.0%;  Pred. No. 0;
   Matches 2281;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      125 CCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGCTGCC 184
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2281 CCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGCTGCC 2222

Qy      185 GACGACGACCGCGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATGCAGG 244
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Db     2221 GACGACGACCGCGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATGCAGG 2162

Qy      245 GGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACACTCT 304
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Db     2161 GGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACACTCT 2102
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Qy    305 GCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTT 364
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Db   2101 GCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTT 2042

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Db   2041 GGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGA 1982

Qy    425 CAGAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCAACTT 484
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CAGAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCAACTT 1922

Qy    485 CATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCGCCTT 544
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 CATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCGCCTT 1862

Qy    545 CAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGGAGGA 604
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 CAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGGAGGA 1802

Qy    605 CAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTGT 664
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 CAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTGT 1742

Qy    665 CTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCAT 724
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 CTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCAT 1682

Qy    725 CCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCTGGCT 784
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCTGGCT 1622

Qy    785 GCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTT 844
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 GCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTT 1562

Qy    845 CGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAG 904
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAG 1502

Qy    905 AGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCT 964
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Db   1501 AGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCT 1442

Qy    965 GAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGC 1024
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGC 1382

Qy   1025 GGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCTCCCA 1084
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Db   1381 GGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCTCCCA 1322

Qy   1085 GTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGA 1144
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Db   1321 GTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGA 1262

Qy   1145 ACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTACTTA 1204
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Db   1261   ACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTACTTA 1202

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Qy   1265   GGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCCT 1324
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141   GGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCCT 1082

Qy   1325   GCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCCTTGA 1384
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Db   1081   GCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCCTTGA 1022

Qy   1385   TGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGCTGT 1444
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Db   1021   TGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGCTGT 962

Qy   1445   GGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACCCTGA 1504
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Qy   1505   ACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCTCAGG 1564
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Qy   1565   AGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGT 1624
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Db    841   AGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGT 782

Qy   1625   CCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCCTGTC 1684
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Qy   1685   TGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGGCATG 1744
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Db    721   TGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGGCATG 662

Qy   1745   TGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTAAAGA 1804
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Qy   1805   AGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCTTGGC 1864
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Db    601   AGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCTTGGC 542

Qy   1865   CTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAA 1924
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541   CTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAA 482

Qy   1925   TGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGGCAAC 1984
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481   TGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGGCAAC 422

Qy   1985   TGAGAATGGCTTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACCCT 2044
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Db    421 TGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACCCT 362

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          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGACCAG 302

Qy   2105 GGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCACTGT 2164
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCACTGT 242

Qy   2165 CACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATT 2224
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Qy   2225 GAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAA 2284
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Db    181 GAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAA 122

Qy   2285 GGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAG 2344
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Db    121 GGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAG 62

Qy   2345 TGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGG 2404
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Db     61 TGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGG 2

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Db      1 C 1
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RESULT 11
AX528269

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LOCUS       AX528269                2271 bp    DNA     linear   PAT 21-NOV-2002
DEFINITION  Sequence 7 from Patent WO0206339.
ACCESSION   AX528269
VERSION     AX528269.1  GI:25172572
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Spaderna,S.K., Tchernev,V., Liu,X., Shenoy,S., Spytek,K.,
            Zerhusen,B., Patturajan,M., Taupier,R.J., Rastelli,L., Grosse,W.M.,
            Szekeres,E.S., Alsobrook,J.I., Lepley,D.M., Shen,L., Burgess,C.E.,
            Shimkets,R.A. and Padigaru,M.
  TITLE     Proteins and nucleic acids encoding same
  JOURNAL   Patent: WO 0206339-A 7 24-JAN-2002;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN
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Query Match              70.9%;   Score 2228.4;   DB 6;   Length 2271;
Best Local Similarity    98.9%;   Pred. No. 0;
Matches 2260;  Conservative      0;  Mismatches   11;  Indels   15;  Gaps    1;

Qy      105 ATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAA 164
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 ATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAA 60

Qy      165 CTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCC 224
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 CTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCC 120

Qy      225 AGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGC 284
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 AGGGTCAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGC 180

Qy      285 CTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCT 344
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 CTCCAGGATTTTGACACTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCT 240

Qy      345 CGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATG 404
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 CGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATG 300

Qy      405 ATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAAT 464
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 ATACCGTGGCCAGCCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAAT 360

Qy      465 GAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTAC 524
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 GAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTAC 420

Qy      525 ACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTAC 584
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Db      421 ACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTAC 480

Qy      585 CTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCC 644
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Db      481 CTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCC 540

Qy      645 GCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAAC 704
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Db      541 GCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAAC 600

Qy      705 TTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACC 764
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 TTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACC 660

Qy      765 GACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACC 824
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Db      661 GACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACC 720

Qy      825 CAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTC 884
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 CAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTC 780

Qy      885 CACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAG 944
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Db      781  CACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAG 840

Qy      945  AAGAAGTGGACCACCTTCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCC 1004
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841  AAGAAGTGGACCACCTTCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCC 900

Qy     1005  TTCAACGTCATCCGCCACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATC 1064
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901  TTCAACGTCATCCGCCACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATC 960

Qy     1065  TACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCC 1124
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Db      961  TACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCC 1020

Qy     1125  TTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAA 1184
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Db     1021  TTCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAA 1080

Qy     1185  ACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCA 1244
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Db     1081  ACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCA 1140

Qy     1245  GTGGGCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAG 1304
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Db     1141  GTGGGCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAG 1200

Qy     1305  CAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTG 1364
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Db     1201  CAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTG 1260

Qy     1365  GAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACA 1424
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Db     1261  GAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCAGTACA 1320

Qy     1425  GGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATT 1484
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Db     1321  GGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATT 1380

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Db     1441  GTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTAT 1500

Qy     1605  GAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCC 1664
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Db     1501  GAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCC 1560

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Db     1561  CGACTCTGCTCTCT---------------TAGGAACTCCTGGAAGCAGGACATGGAGCGG 1605

Qy     1725  GGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGC 1784
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Db      1606 GGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGC 1665

Qy      1785 CGCCCGCAAATCATTAAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGC 1844
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Db      1726 CCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAA 1785

Qy      1905 GCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGT 1964
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Db      1786 GCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGT 1845

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Qy      2025 GACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCAT 2084
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1906 GACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCAT 1965

Qy      2085 GTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTAC 2144
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Db      2146 ACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAG 2205

Qy      2325 GAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTA 2384
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Db      2206 GAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTA 2265

Qy      2385 GCTTAA 2390
             ||||||
Db      2266 GCTTAA 2271


RESULT 12
AX879068
LOCUS       AX879068              1838 bp    DNA       linear   PAT 17-DEC-2003
DEFINITION  Sequence 13973 from Patent EP1074617.
ACCESSION   AX879068
VERSION     AX879068.1  GI:40033804
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Query Match   58.4%; Score 1834.8; DB 6; Length 1838;
Best Local Similarity   99.9%; Pred. No. 0;
Matches 1836; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

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Qy     1479 GAGATTCAGCTGTTCCCTGACCCTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAG 1538
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Db      181 GAGATTCAGCTGTTCCCTGACCCTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAG 240

Qy     1539 GGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGT 1598
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 GGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGT 300

Qy     1599 GTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCT 1658
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Db      301 GTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCT 360

Qy     1659 GAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATG 1718
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 GAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATG 420
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Qy   1719 GAGCGGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCT 1778
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Db    421 GAGCGGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCT 480

Qy   1779 CAGAGCCGCCCGCAAATCATTAAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTC 1838
           |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db    481 CAGAGCCGCCCGCAAATCATTAAAGAAGTCCTGGCTGTCCCTAACTCCATCCTGGAGCTC 540

Qy   1839 CCCTGCCCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTC 1898
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CCCTGCCCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTC 600

Qy   1899 CCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTT 1958
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Db    601 CCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTT 660

Qy   1959 GGGGGTCTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTAC 2018
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Qy   2019 TGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGG 2078
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Qy   2079 GAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAG 2138
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Qy   2139 TCCTACTGGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCC 2198
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Db    841 TCCTACTGGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCC 900

Qy   2199 CTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGC 2258
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Qy   2259 TGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCT 2318
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Qy   2379 GAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGG 2438
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Db   1081 GAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGG 1140

Qy   2439 CTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTC 2498
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Qy   2499 CCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTGATGCACAG 2558
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Db     1261   CAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGG 1320

Qy     2619   GGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGT 2678
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Db     1321   GGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGT 1380

Qy     2679   TCTGGCCATTCCAGGGACCCTCCAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGC 2738
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Db     1381   TCTGGCCATTCCAGGGACCCTCCAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGC 1440

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Db     1441   CTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTAAACAATCATATGCTAACATGC 1500

Qy     2799   CACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAG 2858
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Db     1501   CACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAG 1560

Qy     2859   GGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCA 2918
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Db     1561   GGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCA 1620

Qy     2919   GGAAGTCTTTCCTGAAGTCTGACCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGAT 2978
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1621   GGAAGTCTTCCCTGAAGTCTGACCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGAT 1680

Qy     2979   CCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAG 3038
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Db     1681   CCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAG 1740

Qy     3039   CTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTG 3098
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Db     1741   CTGACCCCTTCACCTCTCCCCCTCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTG 1800

Qy     3099   TCAGAGACTGTTTATTTTTTATTAAAAATATAAGGCTT 3136
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Db     1801   TCAGAGACTGTTTATTTTTTATTAAAAATATAAGGCTT 1838
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RESULT 13
BD157628
LOCUS   BD157628   1838 bp   DNA   linear   PAT 17-JAN-2003
DEFINITION   Primer for synthesizing full-length cDNA and use thereof.
ACCESSION   BD157628
VERSION   BD157628.1 GI:27863386
KEYWORDS   JP 2002191363-A/12471.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1838)
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
               Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
    TITLE   Primer for synthesizing full-length cDNA and use thereof
  JOURNAL   Patent: JP 2002191363-A 12471 09-JUL-2002;
               HELIX RESEARCH INSTITUTE

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ORIGIN


   Query Match          58.4%;  Score 1834.8;  DB 6;  Length 1838;
   Best Local Similarity  99.9%;  Pred. No. 0;
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Qy     1299 GATGAGCAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTT 1358
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Db        1 GATGAGCAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTT 60

Qy     1359 GCAGTGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACC 1418
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Db       61 GCAGTGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACC 120

Qy     1419 ACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAA 1478
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 ACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAA 180

Qy     1479 GAGATTCAGCTGTTCCCTGACCCTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAG 1538
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Db      181 GAGATTCAGCTGTTCCCTGACCCTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAG 240

Qy     1539 GGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGT 1598
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 GGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGT 300

Qy     1599 GTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCT 1658
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 GTCTATGAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCT 360

Qy     1659 GAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATG 1718
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Db      361 GAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATG 420

Qy     1719 GAGCGGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCT 1778
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Db      421 GAGCGGGGGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCT 480
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Qy     1779  CAGAGCCGCCCGCAAATCATTAAAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTC  1838
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Db      481  CAGAGCCGCCCGCAAATCATTAAAGAAGTCCTGGCTGTCCCTAACTCCATCCTGGAGCTC   540

Qy     1839  CCCTGCCCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTC  1898
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      541  CCCTGCCCCCACCTGTCAGCCTTGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTC   600

Qy     1899  CCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTT  1958
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Db      601  CCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTT   660

Qy     1959  GGGGGTCTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTAC  2018
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Db      661  GGGGGTCTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTAC   720

Qy     2019  TGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGG  2078
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      721  TGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGG   780

Qy     2079  GAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAG  2138
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      781  GAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAG   840

Qy     2139  TCCTACTGGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCC  2198
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      841  TCCTACTGGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCC   900

Qy     2199  CTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGC  2258
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Db      901  CTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGC   960

Qy     2259  TGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCT  2318
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Db      961  TGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCT  1020

Qy     2319  CCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACT  2378
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     1021  CCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACT  1080

Qy     2379  GAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGG  2438
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Db     1081  GAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGG  1140

Qy     2439  CTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTC  2498
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Db     1141  CTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTC  1200

Qy     2499  CCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTGATGCACAG  2558
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Db     1201  CCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTGATGCACAG  1260

Qy     2559  CAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGG  2618
             | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     1261  CAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGG  1320
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Qy    2619 GGGCTACCCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGT 2678
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Qy    2739 CTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTAAACAATCATATGCTAACATGC 2798
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Qy    2799 CACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAG 2858
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Qy    3099 TCAGAGACTGTTTATTTTTTATTAAAAATATAAGGCTT 3136
           ||||||||||||||||||||||||||||||||||||||
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RESULT 14
AK022349
LOCUS   AK022349   1838 bp   mRNA   linear   PRI 01-AUG-2002
DEFINITION   Homo sapiens cDNA FLJ12287 fis, clone MAMMA1001771, moderately
             similar to M.musculus mRNA for semaphorin B.
ACCESSION   AK022349
VERSION   AK022349.1 GI:10433727
KEYWORDS   oligo capping; fis (full insert sequence).
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
             Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H.,
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ORIGIN

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Qy   1359 GCAGTGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACC 1418
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Qy   1419 ACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAA 1478
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Db   121 ACCACAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAA 180

Qy   1479 GAGATTCAGCTGTTCCCTGACCCTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAG 1538
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Qy    1539  GGTGCAGTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGT  1598
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Qy    2019  TGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGG  2078
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Qy    2139  TCCTACTGGCCCCACTTTGTCACTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCC  2198
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RESULT 15
BC025800
LOCUS   BC025800   3159 bp   mRNA   linear   ROD 12-NOV-2003
DEFINITION   Mus musculus sema domain, immunoglobulin domain (Ig), transmembrane
             domain (TM) and short cytoplasmic domain, (semaphorin) 4A, mRNA

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                       (cDNA clone MGC:35988 IMAGE:5102015), complete cds.
ACCESSION    BC025800
VERSION      BC025800.1  GI:19387926
KEYWORDS     MGC.
SOURCE       Mus musculus (house mouse)
  ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE    1  (bases 1 to 3159)
  AUTHORS    Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
             Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
             Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
             Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
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             Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
             Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
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             Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
             Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
             Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
             Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE      Generation and initial analysis of more than 15,000 full-length
             human and mouse cDNA sequences
  JOURNAL    Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   MEDLINE   22388257
   PUBMED    12477932
REFERENCE    2  (bases 1 to 3159)
  AUTHORS    Strausberg,R.
  TITLE      Direct Submission
  JOURNAL    Submitted (11-MAR-2002) National Institutes of Health, Mammalian
             Gene Collection (MGC), Cancer Genomics Office, National Cancer
             Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
             USA
  REMARK     NIH-MGC Project URL: http://mgc.nci.nih.gov
  COMMENT    Contact: MGC help desk
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: Jeffrey E. Green, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Genome Sequence Centre,
             BC Cancer Agency, Vancouver, BC, Canada
             info@bcgsc.bc.ca
             Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
             Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
             Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
             Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
             Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
             Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
             Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
             George Yang, Scott Zuyderduyn, Marco Marra.
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Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 57 Row: j Column: 12
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 7305468.

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ORIGIN
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Query Match   56.0%; Score 1760; DB 10; Length 3159;

Best Local Similarity   76.7%;   Pred. No. 0;
Matches 2356;   Conservative   0;   Mismatches 620;   Indels   94;   Gaps   13;

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Db
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           || || ||| | ||||| || ||||||||| |||||||||||||||||||||| |||||| ||
Db   1632  AGAGTTCCCAGGGCCAATTGCAGTGTCTACGAGAGCTGTGTGGACTGTGTGCTTGCCAGG 1691

Qy   1635  GACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCCAAC 1694
           ||||| |||||||||||||||||||||| || || ||| |||| |||||||| | | | |
Db   1692  GACCCTCACTGTGCCTGGGACCCTGAATCAAGACTCTGCAGCCTTCTGTCTGGCTCTACC 1751

Qy   1695  CTGAACTCCTGGAAGCAGGACATGGAGCGGGGGGAACCCAGAGTGGGCATGTGCCAGTGGC 1754
           || | |||||||||||||||||||||||| || || ||||| ||||||| ||| || |||||
Db   1752  ---AAGCCTTGGAAGCAGGACATGGAACGCGGCAACCCGGAGTGGGTATGCACCCGTGGC 1808
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Qy   1755 CCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTAAAGAAGTCCTGGCT 1814
          ||||||  |||||||| ||||  ||||||||  ||| ||| | |||||||||||||||| |
Db   1809 CCCATGGCCAGGAGCCCCCGGCGTCAGAGCCCCCCTCAACTAATTAAAGAAGTCCTGACA 1868

Qy   1815 GTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCTTGGCCTCTTATTAT 1874
          |||||||||||||||||||||||||| |||||||||||||||||||||| |||||||| |
Db   1869 GTCCCCAACTCCATCCTGGAGCTGCCCTGCCCCCACCTGTCAGCACTGGCCTCTTACCAC 1928

Qy   1875 TGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTC 1934
          |||||||||||| |||    | || ||||||||||| ||| ||||||||||||||||||||
Db   1929 TGGAGTCATGGCCGAGCCAAAATCTCAGAAGCCTCTGCTACCGTCTACAATGGCTCCCTC 1988

Qy   1935 TTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGGCAACTGAGAATGGC 1994
          ||||||| |  ||||||||| || |||||| ||||||||||| |||  ||| ||||| |||
Db   1989 TTGCTGCTGCCGCAGGATGGTGTCGGGGGCCTCTACCAGTGTGTGGCGACTGAGAACGGC 2048

Qy   1995 TTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGACCCTGGCCCTGGAT 2054
          |   ||||||||||| ||||||| ||||| |||||||||||||||| ||||||| |||| 
Db   2049 TACTCATACCCTGTGGTCTCCTATTGGGTAGACAGCCAGGACCAGCCCCTGGCGCTGGAC 2108

Qy   2055 CCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGACCAGGGTCAGTGGT 2114
          ||||| ||||| ||| | ||||| ||| |||| |||||||||| |||||||||| | || 
Db   2109 CCTGAGCTGGCGGGCGTTCCCCGTGAGCGTGTGCAGGTCCCGCTGACCAGGGTCGGAGGC 2168

Qy   2115 GGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCACTGTCACTGTCCTC 2174
          || ||   ||  ||||||||||| |||||||||||||| ||| ||| || || |||||||
Db   2169 GGAGCTTCCATGGCTGCCCAGCGGTCCTACTGGCCCCATTTTCTCATCGTTACCGTCCTC 2228

Qy   2175 TTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCCCATTGAGAGCACTC 2234
          | ||| | ||||| |     |||| ||||    ||||| | || ||||||| || | || |
Db   2229 CTGGCCATCGTGCTCCTGGGAGTGCTCACTCTCCTCCTCGCTTCCCCACTGGGGGCGCTG 2288

Qy   2235 CGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCCGTTA 2294
          |||||||||||| |||||||||||||||| |||| ||| ||| ||| ||||| || |
Db   2289 CGGGCTCGGGGTAAGGTTCAGGGCTGTGGGATGCTGCCCCCCAGGGGAAAGGCTCCACTG 2348

Qy   2295 AGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTGCCAGTGATGTGGAC 2354
          ||||| || || ||||||||| ||| |||||| | || |||||||||||||||| || ||
Db   2349 AGCAGGGACCAGCACCTCCAGCCCTCCAAGGACCACAGGACCTCTGCCAGTGACGTAGAT 2408

Qy   2355 GCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCACAGGCCGGGGCT-- 2412
          || |||||||||||  || ||| | || || |||||||||||          ||| |||
Db   2409 GCCGACAACAACCATCTGGGCGCCGAAGTGGCTTAAACAGGGACACAGATCCGCAGCTGA 2468

Qy   2413 GCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGA 2472
          || | ||| || |||||| || ||||| |||  ||
Db   2469 GCAGAGCAAGCCACTGGCCTTGTTGGCTATGC---------------------------- 2500

Qy   2473 CAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTG 2532
             |||    | | |   || |    | |||| || ||||||  || |||||  || ||||
Db   2501 ---CAGGCACAGTGCCACTCTGACCAGGGTAGGAGGCTCTCCTGCTAACGTGTGTCACCT 2557

Qy   2533 ATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCA 2592
          |   ||| ||| |||                    |||||||| ||||||||| |||| |
Db   2558 ACAGCACCCAGTAGG-------------------TCCTCCCCTGTGGGACTCTCTTCTGCAA 2600
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Qy    2593 AGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCCTACACTGATATT 2652
           ||  |||  |||                             |||  |||||  |  |   |||   |
Db    2601 GCACATTGGGCTGTCT-------------------CCATACCTGTACTTGTGCTGTGACA 2641

Qy    2653 GAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAACACAGT 2712
           |  |  | |  || ||| | |||  ||  ||     |||  |  |||||| | |||| |
Db    2642 GGAAGAGCCAGACAGGTTTCTTTGATTTTGATTGACCCAAGAGCCCTCCTGTAACAAACG 2701

Qy    2713 GTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAAAC 2772
           || ||     ||     |||        |  |||  ||  |||| | |||  | ||| | ||  |
Db    2702 TGCTCCAGGAGACCATGAAAGGTGTGGCTGTCTGGGATTCTGTGGTGACAAAC-CTAAGC 2760

Qy    2773 ATCTAAACAATCATATGCTA-------ACATGCCACTCCTGGAAACTCCACTCT----GA 2821
           ||| | ||| |       |||| | |  |||  |             ||||||        |
Db    2761 ATCCGAGCAAGCTGGGGCTATTCCTGCAAACTCCATCCTGAACGCTGTCACTCTAGAAGC 2820

Qy    2822 AGCTGCCGCTTTGGACACCAACACTCCCTTC-TCCCAGGGTCATGCAGGGATCTGCTCCC 2880
           |||||| |||||| |||||| ||||||  | |  |||| | ||||||  |     |  | |||  || |||
Db    2821 AGCTGCTGCTTTGAACACCAGCCCACCCTCCTTCCCAAGAGTCTCTATGGAGTTGGCCCC 2880

Qy    2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940
           |  || |||| ||||||||| |||  |||      |||  |   ||||||| | |||||||| |
Db    2881 TTGTGTTTCCTTTACCAGTCATGCCATACTGTTT---GGGAAGTCATCTCTGAAGTCTAA 2937

Qy    2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCT---TCTGCCCTGGC-AGA 2996
           |||||||  ||||||||||||||||||| ||  ||||  |  |  |    |||||||||||| |||
Db    2938 CCACCTTCCTTCTTGCTTCAGTTTGGACAGATTGTTATTATTGTCTCTGCCCTGGCTAGA 2997

Qy    2997 ATGGCAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTC 3056
           ||||  ||  ||||||||||||||||| |||  ||  |   |    | |||||||| |     |
Db    2998 ATGGGGGGCATAATCTGAGCCTTGTTCCCTTGTCCAGTGTGGCTGACCCTTGACCTCTT- 3056

Qy    3057 CCCCTCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTT 3116
           ||  |||      |  ||||||||||||||||||||||||||||||||||||||||| ||||   |||||||||
Db    3057 -CCTTCCTCCTCCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCACAGACAATTTATTTT 3115

Qy    3117 TTATTAAAAA 3126
           ||||||||||
Db    3116 TTATTAAAAA 3125


Search completed: May 13, 2004, 13:25:29
Job time : 12086 secs
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OM nucleic - nucleic search, using sw model

Run on: May 13, 2004, 07:57:08 ; Search time 1158 Seconds
                                         (without alignments)
                                         11530.299 Million cell updates/sec

Title: US-10-015-391A-276
Perfect score: 3143
Sequence: 1 gggctgaggcactgagagac.........aaatataaggcttaaaaaaa 3143

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_29Jan04:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002s:*
                 7: geneseqn2003as:*
                 8: geneseqn2003bs:*
                 9: geneseqn2003cs:*
                 10: geneseqn2004s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3143	100.0	3143	3	AAC58392	Aac58392 Human PRO
2	3143	100.0	3143	8	ACD68436	Acd68436 Novel hum
3	3143	100.0	3143	8	ACH04538	Ach04538 Human cDN
4	3143	100.0	3143	8	ACD68082	Acd68082 Novel hum
5	3143	100.0	3143	9	ADC18145	Adc18145 Human PRO
6	3143	100.0	3143	9	ADD70791	Add70791 Human cDN
7	3143	100.0	3143	9	ADD39868	Add39868 Human cDN

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      8    3143   100.0   3143   9   ADD70314              Add70314  Human cDN
      9    3143   100.0   3143   9   ADD38435              Add38435  Human cDN
     10    3143   100.0   3143   9   ADD39391              Add39391  Human cDN
     11    3143   100.0   3143   9   ADD38914              Add38914  Human cDN
     12    3143   100.0   3143   9   ADD40345              Add40345  Human cDN
     13    3143   100.0   3143   9   ADE50566              Ade50566  Human cDN
     14    3143   100.0   3143   9   ADE20178              Ade20178  Human cDN
     15    3143   100.0   3143   9   ADE50089              Ade50089  Human cDN
     16    3143   100.0   3143   9   ADE21647              Ade21647  Human cDN
     17    3131    99.6   3142   3   AAA37100              Aaa37100  Human PRO
     18    3075    97.8   3075   4   AAF54397              Aaf54397  DNA encod
     19   3041.4    96.8   3252   9   ADD67570              Add67570  Human Ly6
     20   3040.8    96.7   3104   5   AAF45125              Aaf45125  Human TAN
     21   3040.8    96.7   3104   7   ABX94103              Abx94103  cDNA enco
     22   3040.8    96.7   3104   7   ACD66780              Acd66780  Secreted
     23   3035.8    96.6   3191   3   AAC69084              Aac69084  Human sec
     24   3029.8    96.4   3042   4   AAK53428              Aak53428  Human pol
     25   3028.2    96.3   3042   7   ABX13628              Abx13628  Human cyt
     26   2860.4    91.0   3146   7   ACC69002              Acc69002  Human neu
     27   2682.2    85.3   2981   9   ADB62165              Adb62165  Human cDN
     28   2476.4    78.8   2768   6   ABS64946              Abs64946  Human cDN
     29    2437    77.5   2745   7   ACC68985              Acc68985  Human neu
     30    2283    72.6   2283   5   AAF45126              Aaf45126  Human TAN
     31    2283    72.6   2283   7   ACD66781              Acd66781  Secreted
  c  32    2281    72.6   2281   6   AAD28945              Aad28945  Human MOL
  c  33    2281    72.6   2281   9   ADD18199              Add18199  Human mol
     34   2228.4    70.9   2271   6   AAD28944              Aad28944  Human MOL
     35   2228.4    70.9   2271   9   ADD18197              Add18197  Human mol
     36   2104.8    67.0   2238   7   ACC69003              Acc69003  Human neu
     37   1834.8    58.4   1838   4   AAH15636              Aah15636  Human cDN
     38   1727.6    55.0   3046   5   AAF45137              Aaf45137  Murine se
     39   1727.6    55.0   3046   5   AAF45140              Aaf45140  Murine DN
     40   1727.6    55.0   3046   7   ACD26369              Acd26369  Secreted
     41   1727.6    55.0   3046   7   ACD26370              Acd26370  Secreted
  c  42   1714.8    54.6   1901   4   AAK53434              Aak53434  Human pol
     43   1015.8    32.3   1674   6   ABK94920              Abk94920  Human nov
     44    925.8    29.5   1730   6   ABS54021              Abs54021  cDNA enco
     45    696.6    22.2    775   4   AAH04875              Aah04875  Human cDN
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<div align="center">ALIGNMENTS</div>

RESULT 1
AAC58392
ID   AAC58392 standard; cDNA; 3143 BP.
XX
AC   AAC58392;
XX
DT   29-JAN-2001 (first entry)
XX
DE   Human PRO1317 nucleotide sequence SEQ ID NO:70.
XX
KW   Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
KW   proliferation; tumourigenesis; identification; cancer; cytostatic;
KW   nootropic; neuroprotective; antiinflammatory; immunosuppressive;
KW   immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;

CC   The present invention describes an isolated antibody that binds to one of
CC   the human PRO proteins designated PRO212, PRO290, PRO341, PRO535, PRO619,
CC   PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009, PRO1025,
CC   PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184, PRO1187,
CC   PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094, PRO2145 OR
CC   PRO2198. PRO antagonists can be used to inhibit tumour cell growth. The
CC   PRO polypeptides and nucleotides are useful in the treatment, diagnosis
CC   and prevention of cancer. The antibodies and other anti-tumour compounds
CC   maybe used to treat various conditions, including those characterised by
CC   overexpression and/or activation of the amplified PRO genes. Exemplary
CC   conditions or disorders to be treated with such antibodies and other
CC   compounds include benign or malignant tumours (e.g., renal, liver,
CC   kidney, bladder, breast, gastric, ovarian, colorectal, prostate,
CC   pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas,
CC   glioblastomas, and various head and neck tumours), leukaemias and
CC   lymphoid malignancies, other disorders such as neuronal, glial,
CC   astrocytal, hypothalamic and other glandular, macrophagal, epithelial,
CC   stromal and blastocoelic disorders, and inflammatory, angiogenic and
CC   immunologic disorders. AAC58242 to AAC58366 represent PCR primers and
CC   hybridisation probes used in the isolation of the human PRO sequences.
CC   AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human PRO
CC   polynucleotide and protein sequences given in the exemplification of the

```
CC    present invention
XX
SQ    Sequence 3143 BP; 656 A; 963 C; 828 G; 696 T; 0 U; 0 Other;

     Query Match              100.0%;   Score 3143;   DB 3;   Length 3143;
     Best Local Similarity    100.0%;   Pred. No. 0;
     Matches 3143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;


Qy          1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60

Qy         61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120

Qy        121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180

Qy        181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240

Qy        241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300

Qy        301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360

Qy        361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420

Qy        421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480

Qy        481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540

Qy        541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600

Qy        601 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660

Qy        661 CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC 720

Qy        721 CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT 780
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                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721  CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT  780

Qy      781  GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT  840
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781  GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT  840

Qy      841  TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  900
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841  TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  900

Qy      901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960

Qy      961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020

Qy     1021  ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT  1080
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021  ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT  1080

Qy     1081  CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA  1140
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081  CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA  1140

Qy     1141  TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA  1200
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141  TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA  1200

Qy     1201  CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG  1260
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201  CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG  1260

Qy     1261  ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC  1320
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1261  ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC  1320

Qy     1321  CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC  1380
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1321  CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC  1380

Qy     1381  TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG  1440
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1381  TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG  1440

Qy     1441  CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC  1500
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1441  CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC  1500

Qy     1501  CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT  1560
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1501  CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT  1560

Qy     1561  CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT  1620
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    1561  CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT  1620

Qy    1621  GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC  1680
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621  GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC  1680

Qy    1681  TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG  1740
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RESULT 3
ACH04538
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ID   ACH04538 standard; cDNA; 3143 BP.
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DT   01-OCT-2003   (first entry)
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DE   Human cDNA encoding secreted/transmembrane protein PRO1317.
XX
KW   Human; ss; gene; secreted protein; transmembrane protein; PRO; vulnerary;
KW   cardiant; antidiabetic; anorectic; antiarthritic; angiogenesis; cancer;
KW   adrenal cortical capillary; endothelial cell growth; wound healing;
KW   stimulated T-lymphocyte proliferation; immune response suppression;
KW   neonatal heart hypertrophy; cardiac insufficiency disorder;
KW   vascular endothelial growth factor; inflammation; mononuclear cell;
KW   eosinophil; diabetes; obesity; or hyper-insulinaemia; hypo-insulinaemia;
KW   chondrocyte redifferentiation; bone disorder; cartilage disorder;
KW   sports injury; arthritis.
XX
OS   Homo sapiens.
XX
PN   US2003044841-A1.
XX
PD   06-MAR-2003.
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PF   06-DEC-2001; 2001US-00006856.
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Qy   1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860
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RESULT 4
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ID    ACD68082 standard; cDNA; 3143 BP.
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AC    ACD68082;
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DT    17-SEP-2003  (first entry)
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DE    Novel human secreted and transmembrane protein PRO1317 cDNA.
XX
KW    Human; secreted and transmembrane protein; PRO; gene therapy; vaccine;
KW    tissue typing; chromosome identification; vaccine; gene; ss.
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OS    Homo sapiens.
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PI    Gao W,  Goddard A,  Godowski PJ,  Grimaldi JC,  Gurney AL,  Hillan KJ;
PI    Pan J,  Paoni NF,  Roy MA,  Smith V,  Stewart TA,  Tumas D,  Watanabe CK;
PI    Williams PM,  Wood WI;
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DR    WPI; 2003-585292/55.
DR    P-PSDB; AB033537.
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RESULT 5
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KW    Human; PRO; gene; ss; protein electrophoresis; chromosome mapping;
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Db    841  TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  900

Qy    901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960
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Db    901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960

Qy    961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1021  ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT  1080
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Db   1021  ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT  1080

Qy   1081  CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA  1140
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Db   1081  CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA  1140

Qy   1141  TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA  1200
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Db   1141  TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA  1200
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Qy  2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220
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RESULT 6
ADD70791
ID    ADD70791 standard; cDNA; 3143 BP.
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AC    ADD70791;
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DT    15-JAN-2004   (first entry)
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DE    Human cDNA encoding secreted/transmembrane protein PRO1317.
XX
KW    Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW    immune response; cardiac insufficiency disorder; calcium flux;
KW    umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW    arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW    Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW    dermatitis; herpetiformis; Crohn's disease; thalassaemia.
XX
OS    Homo sapiens.
XX
PN    US2003099625-A1.
XX
PD    29-MAY-2003.
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PF    12-DEC-2001; 2001US-00015386.
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XX
PA    (GETH ) GENENTECH INC.
XX
PI    Baker KP,  Botstein D,  Desnoyers L,  Eaton DL,  Ferrara N,  Fong S;
PI    Gao W,  Goddard A,  Godowski PJ,  Grimaldi JC,  Gurney AL,  Hillan KJ;
PI    Pan J,  Paoni NF,  Roy MA,  Smith V,  Stewart TA,  Tumas D,  Watanabe CK;
PI    Williams PM,  Wood WI;
XX
DR    WPI; 2003-874602/81.
DR    P-PSDB; ADD70792.
XX
PT    Novel isolated PRO polypeptides e.g., PRO1130, PRO1275, PRO1418, PRO1555,
PT    PRO1787 affect glucose or free fatty acid (FFA) uptake by skeletal muscle
PT    cells and are useful for treating diabetes or hyper- or hypo-insulinemia.
XX
PS    Claim 2; SEQ ID NO 276; 553pp; English.
XX
CC    The invention relates to an isolated PRO polypeptide (secreted or

      Query Match            100.0%;  Score 3143;  DB 9;  Length 3143;
      Best Local Similarity  100.0%;  Pred. No. 0;
      Matches 3143;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy        1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60
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Db     61   ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC   120

Qy    121   TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC   180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121   TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC   180

Qy    181   TGCCGACGACGACCGCGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG   240
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181   TGCCGACGACGACCGCGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG   240

Qy    241   CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA   300
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241   CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA   300

Qy    301   CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG   360
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301   CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG   360

Qy    361   CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA   420
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361   CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA   420

Qy    421   GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA   480
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421   GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA   480

Qy    481   ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG   540
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481   ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG   540

Qy    541   CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG   600
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541   CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG   600

Qy    601   AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG   660
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601   AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG   660

Qy    661   CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC   720
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661   CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC   720

Qy    721   CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT   780
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721   CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT   780

Qy    781   GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT   840
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781   GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT   840

Qy    841   TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG   900
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      841  TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  900

Qy      901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960

Qy      961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020

Qy     1021  ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT  1080
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021  ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT  1080

Qy     1081  CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA  1140
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081  CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA  1140

Qy     1141  TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA  1200
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141  TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA  1200

Qy     1201  CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG  1260
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201  CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG  1260

Qy     1261  ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC  1320
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1261  ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC  1320

Qy     1321  CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC  1380
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1321  CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC  1380

Qy     1381  TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG  1440
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1381  TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG  1440

Qy     1441  CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC  1500
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1441  CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC  1500

Qy     1501  CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT  1560
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1501  CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT  1560

Qy     1561  CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT  1620
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1561  CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT  1620

Qy     1621  GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC  1680
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1621  GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC  1680

Qy     1681  TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG  1740
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1681  TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG  1740
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Qy   1741 CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800

Qy   1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860

Qy   1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920

Qy   1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980

Qy   1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040

Qy   2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100

Qy   2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160

Qy   2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220

Qy   2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280

Qy   2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340

Qy   2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400

Qy   2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460

Qy   2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520

Qy   2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580
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Qy    2581  TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2581  TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640

Qy    2641  TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2641  TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700

Qy    2701  CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2701  CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760

Qy    2761  TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2761  TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820

Qy    2821  AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2821  AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880

Qy    2881  TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940
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Db    2881  TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940

Qy    2941  CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2941  CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000

Qy    3001  CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3001  CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060

Qy    3061  TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3061  TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120

Qy    3121  TAAAAATATAAGGCTTAAAAAAA 3143
             |||||||||||||||||||||||
Db    3121  TAAAAATATAAGGCTTAAAAAAA 3143
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RESULT 7
ADD39868
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ID    ADD39868 standard; cDNA; 3143 BP.
XX
AC    ADD39868;
XX
DT    15-JAN-2004  (first entry)
XX
DE    Human cDNA encoding secreted/transmembrane protein PRO1317.
XX
KW    Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW    immune response; cardiac insufficiency disorder; calcium flux;
KW    umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW    arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW    Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW    dermatitis; herpetiformis; Crohn's disease; thalassaemia.
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XX
OS   Homo sapiens.
XX
PN   US2003083462-A1.
XX
PD   01-MAY-2003.
XX
PF   10-DEC-2001; 2001US-00013913.
XX
PR   05-JAN-1999;    99WO-US000106.
PR   01-SEP-1999;    99WO-US020111.
PR   15-SEP-1999;    99WO-US021194.
PR   30-NOV-1999;    99WO-US028313.
PR   02-DEC-1999;    99WO-US028551.
PR   16-DEC-1999;    99WO-US030095.
PR   05-JAN-2000;  2000WO-US000219.
PR   06-JAN-2000;  2000WO-US000376.
PR   11-FEB-2000;  2000WO-US003565.
PR   18-FEB-2000;  2000WO-US004342.
PR   24-FEB-2000;  2000WO-US005004.
PR   02-MAR-2000;  2000WO-US005841.
PR   15-MAR-2000;  2000WO-US006884.
PR   17-MAY-2000;  2000WO-US013705.
PR   22-MAY-2000;  2000WO-US014042.
PR   30-MAY-2000;  2000WO-US014941.
PR   02-JUN-2000;  2000WO-US015264.
PR   23-AUG-2000;  2000WO-US023522.
PR   24-AUG-2000;  2000WO-US023328.
PR   08-NOV-2000;  2000WO-US030952.
PR   10-NOV-2000;  2000WO-US030873.
PR   01-DEC-2000;  2000WO-US032678.
PR   28-FEB-2001;  2001WO-US006520.
PR   01-MAR-2001;  2001WO-US006666.
PR   01-JUN-2001;  2001WO-US017800.
PR   20-JUN-2001;  2001WO-US019692.
PR   29-JUN-2001;  2001WO-US021066.
PR   09-JUL-2001;  2001WO-US021735.
PR   04-SEP-2001;  2001US-00946374.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Botstein D,  Desnoyers L,  Eaton DL,  Ferrara N,  Fong S;
PI   Gao W,  Goddard A,  Godowski PJ,  Grimaldi JC,  Gurney AL,  Hillan KJ;
PI   Pan J,  Paoni NF,  Roy MA,  Smith V,  Stewart TA,  Tumas D,  Watanabe CK;
PI   Williams PM,  Wood WI;
XX
DR   WPI; 2003-755122/71.
DR   P-PSDB; ADD39869.
XX
PT   New secreted and transmembrane PRO polypeptides useful for treating
PT   cancers, kidney disorders, Crohn's disease, diabetes mellitus, hyper- or
PT   hypo-insulinemia, sports injuries and arthritis.
XX
PS   Claim 2; SEQ ID NO 276; 557pp; English.
XX
CC   The invention relates to an isolated PRO polypeptide (secreted or
CC   transmembrane protein) having at least 80% amino acid sequence identity
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CC to an amino acid sequence chosen from 123 fully defined sequences as
CC given in the specification (including their extracellular domains either
CC or without their associated signal peptides. Also include are the
CC nucleotide (NA)sequences encoding PRO, a vector comprising the PRO NA, a
CC host cell comprising the vector, producing PRO, a chimaeric molecule
CC comprising PRO fused to a heterologous amino acid sequence, and an anti-
CC PRO antibody. Pro is useful as molecular weight markers for protein
CC electrophoresis and also for chromosome identification. PRO is also
CC useful for tissue typing. PRO and PRO NA are useful as hybridisation
CC probes for a cDNA library to isolate the full-length PRO cDNA. PRO NA is
CC useful for generating transgenic animals or knock-out animals which are
CC useful in development and screening useful reagents. PRO NA is also
CC useful in gene therapy. PRO1244, PRO1286 and PRO1303 polypeptides are
CC useful for treating cancerous tumours. PRO1250, PRO1418 and PRO1410
CC polypeptides are useful for suppressing immune response. PRO1246
CC polypeptide is useful for treating cardiac insufficiency disorders.
CC PRO1246 polypeptide is also useful for treating tumours. PRO1246 and
CC PRO1561 polypeptide are useful for stimulating calcium flux in human
CC umbilical vein endothelial cells. PRO1265, PRO1250 and PRO1474
CC polypeptides are useful for treating bone and/or cartilage disorders
CC (e.g., arthritis) and wound healing. PRO1130, PRO1275 and PRO1418
CC polypeptides are useful for treating diabetes in skeletal muscle cells
CC and obesity. PRO1265, PRO1244 and PRO1382 polypeptides are useful for
CC treating Berger disease or other nephropathies associated with Schonlein-
CC Henoch purpura, coeliac disease, dermatitis, herpetiformis or Crohn's
CC disease. PRO1478, PRO1265, PRO1412, PRO1279, PRO1304, PRO1306, PRO1418,
CC PRO1410 and PRO1575 are useful in treating thalassaemias. The present
CC sequence encodes a PRO protein of the invention.
XX
SQ Sequence 3143 BP; 656 A; 963 C; 828 G; 696 T; 0 U; 0 Other;

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     Query Match              100.0%;  Score 3143;  DB 9;   Length 3143;
     Best Local Similarity    100.0%;  Pred. No. 0;
     Matches 3143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;


Qy          1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60


Qy         61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120


Qy        121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180


Qy        181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240


Qy        241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300


Qy        301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db     301  CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG  360

Qy     361  CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361  CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA  420

Qy     421  GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421  GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA  480

Qy     481  ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481  ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG  540

Qy     541  CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541  CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG  600

Qy     601  AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG  660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601  AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG  660

Qy     661  CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC  720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661  CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC  720

Qy     721  CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT  780
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Db     721  CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT  780

Qy     781  GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT  840
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Db     781  GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT  840

Qy     841  TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  900
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Db     841  TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  900

Qy     901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960

Qy     961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020
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Db     961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020

Qy    1021  ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT  1080
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Db    1021  ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT  1080

Qy    1081  CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA  1140
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Db    1081  CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA  1140

Qy    1141  TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA  1200
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Qy   1321 CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC 1380
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Qy   1381 TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG 1440
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Qy   1561 CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT 1620
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Db    2881  TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940

Qy    2941  CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000
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RESULT 8
ADD70314
ID    ADD70314 standard; cDNA; 3143 BP.
XX
AC    ADD70314;
XX
DT    15-JAN-2004   (first entry)
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DE    Human cDNA encoding secreted/transmembrane protein PRO1317.
XX
KW    Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW    immune response; cardiac insufficiency disorder; calcium flux;
KW    umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW    arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW    Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW    dermatitis; herpetiformis; Crohn's disease; thalassaemia.
XX
OS    Homo sapiens.
XX
PN    US2003054406-A1.
XX
PD    20-MAR-2003.
XX
PF    06-DEC-2001; 2001US-00006818.
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PR    30-DEC-1998;    98US-0114223P.
PR    05-JAN-1999;    99WO-US000106.
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PR    15-SEP-1999;   99WO-US021194.
PR    29-OCT-1999;   99US-0162506P.
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PR    02-DEC-1999;   99WO-US028551.
PR    16-DEC-1999;   99WO-US030095.
PR    05-JAN-2000; 2000WO-US000219.
PR    06-JAN-2000; 2000WO-US000376.
PR    11-FEB-2000; 2000WO-US003565.
PR    18-FEB-2000; 2000WO-US004342.
PR    24-FEB-2000; 2000WO-US005004.
PR    02-MAR-2000; 2000WO-US005841.
PR    15-MAR-2000; 2000WO-US006884.
PR    17-MAY-2000; 2000WO-US013705.
PR    22-MAY-2000; 2000WO-US014042.
PR    30-MAY-2000; 2000WO-US014941.
PR    02-JUN-2000; 2000WO-US015264.
PR    23-AUG-2000; 2000WO-US023522.
PR    24-AUG-2000; 2000WO-US023328.
PR    08-NOV-2000; 2000WO-US030952.
PR    10-NOV-2000; 2000WO-US030873.
PR    01-DEC-2000; 2000WO-US032678.
PR    28-FEB-2001; 2001WO-US006520.
PR    01-MAR-2001; 2001WO-US006666.
PR    01-JUN-2001; 2001WO-US017800.
PR    20-JUN-2001; 2001WO-US019692.
PR    29-JUN-2001; 2001WO-US021066.
PR    09-JUL-2001; 2001WO-US021735.
PR    04-SEP-2001; 2001US-00946374.
XX
PA    (GETH ) GENENTECH INC.
XX
PI    Baker KP,  Botstein D,  Desnoyers L,  Eaton DL,  Ferrara N,  Fong S;
PI    Gao W,  Goddard A,  Godowski PJ,  Grimaldi JC,  Gurney AL,  Hillan KJ;
PI    Pan J,  Paoni NF,  Roy MA,  Smith V,  Stewart TA,  Tumas D,  Watanabe CK;
PI    Williams PM,  Wood WI;
XX
DR    WPI; 2003-708344/67.
DR    P-PSDB; ADD70315.
XX
PT    Novel isolated PRO polypeptide useful for tissue typing, modulating
PT    biological activity of cell, as molecular weight markers in protein
PT    electrophoresis, for treating arthritis, tumor.
XX
PS    Claim 2; SEQ ID NO 276; 549pp; English.
XX
CC    The invention relates to an isolated PRO polypeptide (secreted or

  Query Match            100.0%;  Score 3143;  DB 9;  Length 3143;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 3143;  Conservative   0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60
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Qy    1741 CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800
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RESULT 9
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ID   ADD38435 standard; cDNA; 3143 BP.
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AC   ADD38435;
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DT   15-JAN-2004 (first entry)
XX
DE   Human cDNA encoding secreted/transmembrane protein PRO1317.
XX
KW   Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW   immune response; cardiac insufficiency disorder; calcium flux;
KW   umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW   arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW   Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW   dermatitis; herpetiformis; Crohn's disease; thalassaemia.

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PD    22-MAY-2003.
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PF    07-DEC-2001; 2001US-00012755.
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PR    22-DEC-1998;    98US-0113296P.
PR    30-DEC-1998;    98US-0114223P.
PR    05-JAN-1999;    99WO-US000106.
PR    16-APR-1999;    99US-0129674P.
PR    23-JUN-1999;    99US-0141037P.
PR    20-JUL-1999;    99US-0144758P.
PR    26-JUL-1999;    99US-0145698P.
PR    01-SEP-1999;    99WO-US020111.
PR    15-SEP-1999;    99WO-US021194.
PR    29-OCT-1999;    99US-0162506P.
PR    30-NOV-1999;    99WO-US028313.
PR    02-DEC-1999;    99WO-US028551.
PR    16-DEC-1999;    99WO-US030095.
PR    05-JAN-2000; 2000WO-US000219.
PR    06-JAN-2000; 2000WO-US000376.
PR    11-FEB-2000; 2000WO-US003565.
PR    18-FEB-2000; 2000WO-US004342.
PR    24-FEB-2000; 2000WO-US005004.
PR    02-MAR-2000; 2000WO-US005841.
PR    15-MAR-2000; 2000WO-US006884.
PR    17-MAY-2000; 2000WO-US013705.
PR    22-MAY-2000; 2000WO-US014042.
PR    30-MAY-2000; 2000WO-US014941.
PR    02-JUN-2000; 2000WO-US015264.
PR    23-AUG-2000; 2000WO-US023522.
PR    24-AUG-2000; 2000WO-US023328.
PR    08-NOV-2000; 2000WO-US030952.
PR    10-NOV-2000; 2000WO-US030873.
PR    01-DEC-2000; 2000WO-US032678.
PR    28-FEB-2001; 2001WO-US006520.
PR    01-MAR-2001; 2001WO-US006666.
PR    01-JUN-2001; 2001WO-US017800.
PR    20-JUN-2001; 2001WO-US019692.
PR    29-JUN-2001; 2001WO-US021066.
PR    09-JUL-2001; 2001WO-US021735.
PR    04-SEP-2001; 2001US-00946374.
XX
PA    (GETH ) GENENTECH INC.
XX
PI    Baker KP,  Botstein D,  Desnoyers L,  Eaton DL,  Ferrara N,  Fong S;
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PI   Gao W,   Goddard A,   Godowski PJ,   Grimaldi JC,   Gurney AL,   Hillan KJ;
PI   Pan J,   Paoni NF,   Roy MA,   Smith V,   Stewart TA,   Tumas D,   Watanabe CK;
PI   Williams PM,   Wood WI;
XX
XX
PT   Novel isolated PRO polypeptide, useful for treating cancerous tumors,
PT   cardiac insufficiency disorders, wound healing, diabetes mellitus,
PT   thalassemias.
XX
PS   Claim 2; SEQ ID NO 276; 556pp; English.
XX
CC   The invention relates to an isolated PRO polypeptide (secreted or
CC   transmembrane protein) having at least 80% amino acid sequence identity

       Query Match   100.0%;   Score 3143;   DB 9;   Length 3143;
       Best Local Similarity   100.0%;   Pred. No. 0;
       Matches 3143;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60

Qy   61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180
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Qy   241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360
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Db   421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480

Qy   481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540
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Qy   541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600

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Db     541   CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600

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Qy     661   CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC 720
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Db     661   CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC 720

Qy     721   CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT 780
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Db     721   CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT 780

Qy     781   GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT 840
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Db     781   GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT 840

Qy     841   TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG 900
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Qy     901   CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT 960
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     901   CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT 960

Qy     961   TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC 1020
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Qy    1021   ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT 1080
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Db    1021   ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT 1080

Qy    1081   CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA 1140
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Qy    1141   TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA 1200
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1141   TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA 1200

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Db    1201   CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG 1260

Qy    1261   ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC 1320
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1261   ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC 1320

Qy    1321   CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC 1380
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Db     1381 TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG 1440

Qy     1441 CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC 1500
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     1501 CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT 1560
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db     1561 CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT 1620

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Qy     2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100
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Db     2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160

Qy     2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220
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Db     2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220

Qy     2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280
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Db     2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280
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Qy    2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340
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Db    2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340

Qy    2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400
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Qy    2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460
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Db    2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460

Qy    2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520
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Db    2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520

Qy    2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580
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Db    2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580

Qy    2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640
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Qy    2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700
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Db    2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700

Qy    2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760
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Qy    2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820
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Qy    2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880
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Qy    2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940
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Qy    2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000
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Db    2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000

Qy    3001 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060
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Db    3001 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060

Qy    3061 TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3061 TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120
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Qy      3121 TAAAAATATAAGGCTTAAAAAAA 3143
             |||||||||||||||||||||||
Db      3121 TAAAAATATAAGGCTTAAAAAAA 3143
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RESULT 10
ADD39391
ID   ADD39391 standard; cDNA; 3143 BP.
XX
AC   ADD39391;
XX
DT   15-JAN-2004 (first entry)
XX
DE   Human cDNA encoding secreted/transmembrane protein PRO1317.
XX
KW   Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW   immune response; cardiac insufficiency disorder; calcium flux;
KW   umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW   arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW   Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW   dermatitis; herpetiformis; Crohn's disease; thalassaemia.
XX
OS   Homo sapiens.
XX
PN   US2003096954-A1.
XX
PD   22-MAY-2003.
XX
PF   07-DEC-2001; 2001US-00011671.
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RESULT 11
ADD38914

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DT   15-JAN-2004  (first entry)
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DE   Human cDNA encoding secreted/transmembrane protein PRO1317.
XX
KW   Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW   immune response; cardiac insufficiency disorder; calcium flux;
KW   umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW   arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW   Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW   dermatitis; herpetiformis; Crohn's disease; thalassaemia.
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XX
PA    (GETH ) GENENTECH INC.
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PI    Baker KP,  Botstein D,  Desnoyers L,  Eaton DL,  Ferrara N,  Fong S;
PI    Gao W,  Goddard A,  Godowski PJ,  Grimaldi JC,  Gurney AL,  Hillan KJ;
PI    Pan J,  Paoni NF,  Roy MA,  Smith V,  Stewart TA,  Tumas D,  Watanabe CK;
PI    Williams PM,  Wood WI;
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DR    WPI; 2003-765477/72.
DR    P-PSDB; ADD38915.
XX
PT    New isolated PRO polypeptide such as PRO1560, PRO444, PRO1018, PRO1773,
PT    PRO1244, PRO1246, useful for treating cancerous tumors, cardiac
PT    insufficiency disorders, wound healing, Crohn's disease, celiac disease.
XX
PS    Claim 2; SEQ ID NO 276; 555pp; English.
XX
CC    The invention relates to an isolated PRO polypeptide (secreted or
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Query Match              100.0%;  Score 3143;  DB 9;  Length 3143;
Best Local Similarity    100.0%;  Pred. No. 0;
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Db     3121 TAAAAATATAAGGCTTAAAAAAA 3143


RESULT 12
ADD40345
ID   ADD40345 standard; cDNA; 3143 BP.
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AC   ADD40345;
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DT   15-JAN-2004  (first entry)
XX
DE   Human cDNA encoding secreted/transmembrane protein PRO1317.
XX
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KW    Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW    immune response; cardiac insufficiency disorder; calcium flux;
KW    umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW    arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW    Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW    dermatitis; herpetiformis; Crohn's disease; thalassaemia.
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OS    Homo sapiens.
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PN    US2003082627-A1.
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PD    01-MAY-2003.
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PF    06-DEC-2001; 2001US-00006117.
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PR    06-JAN-2000;    2000WO-US000376.
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PR    18-FEB-2000;    2000WO-US004342.
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PR    17-MAY-2000;    2000WO-US013705.
PR    22-MAY-2000;    2000WO-US014042.
PR    30-MAY-2000;    2000WO-US014941.
PR    02-JUN-2000;    2000WO-US015264.
PR    23-AUG-2000;    2000WO-US023522.
PR    24-AUG-2000;    2000WO-US023328.
PR    08-NOV-2000;    2000WO-US030952.
PR    10-NOV-2000;    2000WO-US030873.
PR    01-DEC-2000;    2000WO-US032678.
PR    28-FEB-2001;    2001WO-US006520.
PR    01-MAR-2001;    2001WO-US006666.
PR    01-JUN-2001;    2001WO-US017800.
PR    20-JUN-2001;    2001WO-US019692.
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PR   29-JUN-2001; 2001WO-US021066.
PR   09-JUL-2001; 2001WO-US021735.
PR   04-SEP-2001; 2001US-00946374.
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PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Botstein D,  Desnoyers L,  Eaton DL,  Ferrara N,  Fong S;
PI   Gao W,  Goddard A,  Godowski PJ,  Grimaldi JC,  Gurney AL,  Hillan KJ;
PI   Pan J,  Paoni NF,  Roy MA,  Smith V,  Stewart TA,  Tumas D,  Watanabe CK;
PI   Williams PM,  Wood WI;
XX
DR   WPI; 2003-755104/71.
DR   P-PSDB; ADD40346.
XX
PT   New isolated PRO polypeptides such as PRO1560, PRO444, PRO1018, PRO1773,
PT   PRO1244, PRO1246, are useful for treating cancerous tumors and cardiac
PT   insufficiency disorders.
XX
PS   Claim 2; SEQ ID NO 276; 550pp; English.
XX
CC   The invention relates to an isolated PRO polypeptide (secreted or
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     Query Match   100.0%; Score 3143; DB 9; Length 3143;
     Best Local Similarity 100.0%; Pred. No. 0;
     Matches 3143; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy   2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460
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Db   2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460


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RESULT 13
ADE50566
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ID   ADE50566 standard; cDNA; 3143 BP.
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AC   ADE50566;
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DT   29-JAN-2004  (first entry)
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DE   Human cDNA encoding secreted/transmembrane protein PRO1317.
XX
KW   Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW   immune response; cardiac insufficiency disorder; calcium flux;
KW   umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW   arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW   Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW   dermatitis; herpetiformis; Crohn's disease; thalassaemia.
XX
OS   Homo sapiens.
XX
PN   US2003069179-A1.
XX
PD   10-APR-2003.
XX
PF   11-DEC-2001; 2001US-00015393.
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Qy   2221  CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG  2280
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Qy   2281  AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG  2340
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Qy   2461  TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC  2520
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RESULT 14
ADE20178
ID    ADE20178 standard; cDNA; 3143 BP.
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AC    ADE20178;
XX
DT    29-JAN-2004   (first entry)
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DE    Human cDNA encoding secreted/transmembrane protein PRO1317.
XX
KW    Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW    immune response; cardiac insufficiency disorder; calcium flux;
KW    umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW    arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW    Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW    dermatitis; herpetiformis; Crohn's disease; thalassaemia.
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OS    Homo sapiens.
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PA    (GETH ) GENENTECH INC.
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PI    Baker KP,  Botstein D,  Desnoyers L,  Eaton DL,  Ferrara N,  Fong S;
PI    Gao W,  Goddard A,  Godowski PJ,  Grimaldi JC,  Gurney AL,  Hillan KJ;
PI    Pan J,  Paoni NF,  Roy MA,  Smith V,  Stewart TA,  Tumas D,  Watanabe CK;
PI    Williams PM,  Wood WI;
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DR    WPI; 2003-765493/72.
DR    P-PSDB; ADE20179.
XX
PT    New isolated PRO polypeptide useful for tissue typing, modulating
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    Best Local Similarity 100.0%;  Pred. No. 0;
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Qy    1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860

Qy    1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920
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Db    1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920

Qy    1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980

Qy    1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040

Qy    2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100
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Db    2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100
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Qy    2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160
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Qy    2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220
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Qy    2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280
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Qy    2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340
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Qy    2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400
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Db    2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400

Qy    2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460
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Qy    2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520
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Qy    2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640
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Qy    2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760
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Qy    2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820
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Db    2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820

Qy    2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880
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Db    2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880

Qy    2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940
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Db    2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940
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Qy    2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000
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Db    2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000

Qy    3001 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    3061 TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120
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Qy    3121 TAAAAATATAAGGCTTAAAAAAA 3143
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Search completed: May 13, 2004, 10:04:06
Job time : 1169 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 13, 2004, 09:33:13 ; Search time 212 Seconds
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Title: US-10-015-391A-276
Perfect score: 3143
Sequence: 1 gggctgaggcactgagagac.........aaatataaggcttaaaaaaa 3143

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	230	7.3	2433	4	US-09-300-958A-24	Sequence 24, Appl
2	153.4	4.9	4157	4	US-08-556-422A-1	Sequence 1, Appli
3	126	4.0	3524	4	US-09-077-940A-3	Sequence 3, Appli
4	125.4	4.0	3692	4	US-09-077-940A-1	Sequence 1, Appli
5	102	3.2	2278	4	US-09-976-594-1002	Sequence 1002, Ap
6	98.6	3.1	121	4	US-09-833-381-202	Sequence 202, App
7	98.6	3.1	2790	4	US-09-254-594-5	Sequence 5, Appli
8	98.6	3.1	3432	4	US-09-254-594-4	Sequence 4, Appli
9	89.8	2.9	2787	4	US-09-254-594-2	Sequence 2, Appli
10	89.8	2.9	3195	4	US-09-254-594-1	Sequence 1, Appli
11	84.2	2.7	4286	4	US-09-976-594-632	Sequence 632, App

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12    78.6    2.5    3560    1    US-08-121-713D-59        Sequence 59, Appl
13    78.6    2.5    3560    1    US-08-835-268-59         Sequence 59, Appl
14    78.6    2.5    3560    2    US-09-060-692-59         Sequence 59, Appl
15    78.6    2.5    3560    3    US-08-833-391-59         Sequence 59, Appl
16    78.6    2.5    3560    4    US-09-060-610-59         Sequence 59, Appl
17    78.6    2.5    3560    5    PCT-US94-10151A-59       Sequence 59, Appl
18    78.2    2.5    1923    4    US-09-653-274-12         Sequence 12, Appl
19    78.2    2.5    3261    4    US-09-653-274-5          Sequence 5, Appli
20    78.2    2.5    3694    4    US-09-653-274-3          Sequence 3, Appli
21    69.8    2.2    2670    1    US-08-121-713D-61        Sequence 61, Appl
22    69.8    2.2    2670    1    US-08-835-268-61         Sequence 61, Appl
23    69.8    2.2    2670    2    US-09-060-692-61         Sequence 61, Appl
24    69.8    2.2    2670    3    US-08-833-391-61         Sequence 61, Appl
25    69.8    2.2    2670    4    US-09-060-610-61         Sequence 61, Appl
26    69.8    2.2    2670    5    PCT-US94-10151A-61       Sequence 61, Appl
27    63.8    2.0    2601    1    US-08-121-713D-53        Sequence 53, Appl
28    63.8    2.0    2601    1    US-08-835-268-53         Sequence 53, Appl
29    63.8    2.0    2601    2    US-09-060-692-53         Sequence 53, Appl
30    63.8    2.0    2601    3    US-08-833-391-53         Sequence 53, Appl
31    63.8    2.0    2601    4    US-09-060-610-53         Sequence 53, Appl
32    63.8    2.0    2601    5    PCT-US94-10151A-53       Sequence 53, Appl
33    62.6    2.0    7218    1    US-08-232-463-14         Sequence 14, Appl
34    62      2.0    2854    1    US-08-121-713D-57        Sequence 57, Appl
35    62      2.0    2854    1    US-08-835-268-57         Sequence 57, Appl
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37    62      2.0    2854    3    US-08-833-391-57         Sequence 57, Appl
38    62      2.0    2854    4    US-09-060-610-57         Sequence 57, Appl
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40    52.6    1.7    2898    4    US-09-308-179B-2         Sequence 2, Appli
41    50.2    1.6    2504    1    US-08-121-713D-63        Sequence 63, Appl
42    50.2    1.6    2504    1    US-08-835-268-63         Sequence 63, Appl
43    50.2    1.6    2504    2    US-09-060-692-63         Sequence 63, Appl
44    50.2    1.6    2504    3    US-08-833-391-63         Sequence 63, Appl
45    50.2    1.6    2504    4    US-09-060-610-63         Sequence 63, Appl
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ALIGNMENTS

RESULT 1
US-09-300-958A-24
; Sequence 24, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John
; APPLICANT: Trenkle, Thomas
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
; TITLE OF INVENTION: Using Same
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/09/300,958A
; CURRENT FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624

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    Query Match               7.3%;   Score 230;  DB 4;  Length 2433;
    Best Local Similarity   50.2%;   Pred. No. 4.5e-51;
    Matches  906;  Conservative   0;  Mismatches  805;  Indels  93;  Gaps   10;

Qy        301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360
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Qy        361 CCTTGGATATCCAGGATCCAGGGGTCCC---CAGGCTAAAGAACATGATACCGTGGCCAG 417
              |  | | |||| |          | || | ||    | |    | |   | ||| ||||    |
Db        113 CACTTAACAGCAACCTCAGCTTCTTGCCAGGCGGGGAGTACCAAGAGCTACTGTGGAGTG 172

Qy        418 CCAGTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTT 477
              |   || |     |  ||| |     | ||   ||| |||   ||| |    ||   | |||
Db        173 CAGATGCTGACAGGAAGCAGCAGTGCAGCTTCAAGGGCAAGGACCCAAAGCGTGACTGTC 232

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              ||||  ||||          |||| |  |      ||| || ||| ||     |||||| |||||
Db        233 AAAACTACATCAAGATCCTCCTGCCACTCAACAGCAGCCACCTGCTCACCTGTGGCACGG 292

Qy        538 TCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCT 597
              |||||||||||||   ||| | | ||||| |      |     |     |      | |
Db        293 CCGCCTTCAGCCCCCTGTGTGCTTACATTCACATAGCGAGCTTTACTTTAGCCCAAGATG 352

Qy        598 CGGAGGACAAGGTCAT------GGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACA 651
              || | || |||||     ||| || || || || |  | ||||||||||||        ||
Db        353 AGGCCGGTAATGTCATTCTGGAGGATGGCAAGGGTCATTGTCCCTTTGACCCCAACTTCA 412

Qy        652 AGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGG 711
              ||    |||||| | ||||  |||| |||||   ||| ||   ||| || | | | ||||| ||
Db        413 AGTCCACGGCTCTGGTGGTTGATGGTGAGCTGTACACTGGAACAGTCAGTAGCTTCCAGG 472

Qy        712 GCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACT 771
              | | || || | |     || ||| | | | ||| ||  |  ||||||| || | ||
Db        473 GAAACGACCCAGCCATTTCCCGGAGCCAGAGTTCCCGCCC---CACCAAGACTGAGAGCT 529

Qy        772 TCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCG 831
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Qy        832 ------------------------TCTACTTCTTCTTCGAGGAGACAGCCAGCGAGT 864
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Db        590 GCAGCCCCATAGGTGATGATGATAAGATCTACTTCTTCTTCAGCGAGACGGGCCAGGAGT 649

Qy        865 TTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGG 924
              ||||  |||||||||||      |  |  || || || || ||||||| |||    || | ||
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Db    710 GTGGAGAGCGGGTGTTGCAGCAACGCTGGACCTCCTTTCTCAAGGCTCAGCTCCTGTGCT 769

Qy    985 CCCAGCCGGGGCA---GCTGCCCTTCAACGTCATCCGCCACGCGGTCCTGCTCCCCGCCG 1041
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Qy   1096 GCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTTA 1155
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Db    950 ACGGCCTGTACAAGAAAGTAAACAGAGAGACACAGCAGTGGTATACCGAGACCCACCAGG 1009

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Qy   1243 CAGTGGGCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATG 1302
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Db   1070 CGTCCCTGCAGCTCCCAGACCGAGTGCTGAACTTCCTCAAGGATCACTTCTTGATGGATG 1129

Qy   1303 AGCAAGTGGTGGGGACGCCCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAG 1362
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Db   1130 GGCAGGTCCGCAGTCGCCTGCTGCTGCTGCAGCCCAGAGCCCGCTACCAGCGTGTGGCTG 1189

Qy   1363 TGGAGACAGCCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCA 1422
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Db   1190 TGCACCGTGTGCCTGGCCTGCACAG---CACTTATGATGTCCTATTTCTGGGCACTGGTG 1246

Qy   1423 CAGGGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGA 1482
          ||    ||  |||||| || |||   |  || | | | || | | || | | || |||
Db   1247 ATGGCCGCCTGCACAAAGCAGTG---ACCCTGAGCTCCAGAGTCCACATCATTGAGGAGC 1303

Qy   1483 TTCAGCTGTTCCCTGACCCTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTG 1542
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Db   1304 TGCAGATCTTCCCTCAAGGACAGCCTGTGCAGAACCTGCTCTTGGACAGCCATGGGGGAC 1363

Qy   1543 CAGTGTTTGTAGGCTTCTCAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCT 1602
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Db   1364 TGTTGTATGCCTCCTCCCATTCCGGGGTGGTGCAAGTGCCCGTAGCCAACTGCAGCCTGT 1423

Qy   1603 ATGAGAGCTGTGTGGACTGTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGT 1662
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Db   1424 ACCCAACCTGTGGAGACTGCCTCCTGGCTCGAGACCCCTACTGCGCCTGGACTGGCTCTG 1483

Qy   1663 CCCGAACCTGTTGCCTCCTGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGC 1722
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Qy   1957 TTGGGGGTCTCTACCAGTGCTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCT 2016
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Db   1784 GTTTGGGGGTGTTCCAGTGTTGGTCGATAGAAGAAGGATTCCAGCAGCTTGTGGCCAGCT 1843

Qy   2017 ACTG 2020
        ||||
Db   1844 ACTG 1847


RESULT 2
US-08-556-422A-1
; Sequence 1, Application US/08556422A
; Patent No. 6576754
; GENERAL INFORMATION:
;  APPLICANT: HALL, Kathryn T.
;  APPLICANT:  FREEMAN, Gordon J.
;  APPLICANT:  SCHULTZE, Joachim L.
;  APPLICANT:  BOUSSIOTIS, Vassiliki
;  APPLICANT:  NADLER, Lee M.
;  TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES
;  FILE REFERENCE: DFN-005CPA2
;  CURRENT APPLICATION NUMBER: US/08/556,422A
;  CURRENT FILING DATE:  1995-11-09
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;  LENGTH: 4157
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (88)...(2673)
US-08-556-422A-1

  Query Match              4.9%;   Score 153.4;  DB 4;  Length 4157;
  Best Local Similarity   50.0%;   Pred. No. 1.4e-30;
   Matches  743;  Conservative    0;  Mismatches  636;  Indels  108;  Gaps    10;

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Qy    330 CTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGGTCCCC 389
          | ||| | || || || || || ||      || ||| | | | || |     || ||
Db    271 TTGTACATAGGTGCCCGGGAGGC------GGTCTTCGCTGTGAACGCACTCAACATCTCC 324

Qy    390 AGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTT 449
          |    || | || |   ||| || |   ||    |||||     |||||||
Db    325 GAGAAGCAGCATGAGGTGTATTGGAAGGTCTCAGAAGACAAAAAAGCAAATGTGCAGAA 384

Qy    450 AAGAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAAT 509
          ||| |||     || ||||| |||| |||||| ||||| ||| |||     |    ||
Db    385 AAGGGGAAATCAAAACAGACAGAGTGCCTCAACTACATCCGGGTGCTGCAGCCACTCAGC 444

Qy    510 GTCACCCATCTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAA 569
          | |||    || |||  || || || ||| ||| ||   || || ||| |   |   |
Db    445 GCCACTTCCCTTTACGTGTGTGGGACCAACGCATTCCAGCCGGCCTGTGACCACCTGAAC 504

Qy    570 CTTCAAGATTCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAA 629
          | | |   |    | ||  |    || ||          || ||||||  |
Db    505 TTAACATCCTTTAAGTTTCTGGGGAAAAATGAAGAT-----------GGCAAAGGAAGA 552

Qy    630 AGCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCT 689
          | |||||||||| || ||| ||  |||  | | | || |||| |||| |||    ||||
Db    553 TGTCCCTTTGACCCAGCACACAGCTACACATCCGTCATGGTTGATGGAGAACTTTATTCG 612

Qy    690 GGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAG 749
          || ||   | | || || |||| ||||| ||||| |||||| |   || |        |
Db    613 GGGACGTCGTATAATTTTTTGGGAAGTGAACCCATCATCTCCCGAAATTCTTCCCACAGT 672

Qy    750 CCTGTCCTCAAGACCGACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCA 809
          ||| |     |     |   |||   |     | || || ||| |   |  |||| |
Db    673 CCTCTGAGGACAGAATATGCAATCCCTTGGCTGAACGAGCCTAGTTTCGTGTTTGCTGAC 732

Qy    810 GCCATCCCTTCGACCCAGGTC-------------------------GTCTACTTCTTCTTC 845
          | |||| | || | |     ||||||||||||||||||||
Db    733 GTGATCCGAAAAAGCCCAGACAGCCCCGACGGCGAGGATGACAGGGTCTACTTCTTCTTC 792

Qy    846 GAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGA 905
          ||||      |    ||||  ||| ||  | |   ||| | |  |  | ||| | || |||
Db    793 ACGGAGGTGTCTGTGGAGTATGAGTTTGTGTTCAGGGTGCTGATCCCACGGATAGCAAGA 852

Qy    906 GTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTG 965
          || |||||| |||  ||| ||||||| | | ||||||||||| ||||| |||||||||||
Db    853 GTGTGCAAGGGGGACCAGGGCGGCCTGAGGACCTTGCAGAAGAAATGGACCTCCTTCCTG 912

Qy    966 AAGGCCCAGCTGCTCTGCACCCAGCCGG---GGCAGCTGCCCTTCAACGTCATCCGCCAC 1022
          || |||| || || ||||| ||| ||| |   | || ||||||| || | |  |||
Db    913 AAAGCCCGACTCATCTGCTCCCGGCCAGACAGCGGCTTGGTCTTCAATGTGCTGCGGGAT 972

Qy   1023 GCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCTCC 1082
          |  || |||||     || |    | | | || |||| ||| ||||||||||
Db    973 GTCTTCGTGCTCAGGTCCCCGGGCCTGAAGGTGCCTGTGTTCTATGCACTCTTCACCCCA 1032

Qy   1083 CAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATT 1142
          ||| || || |    ||| |          | | | ||| |||| | || | |
Db   1033 CAGCTGAACAACGTGGGGCTGTCGGCAGTGTGCGCCTACAACCTGTC---CACAGCCGAG 1089

Qy   1143 GAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAG---------AAACTTCACGC 1193
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              ||      |||     |  |||||  ||||    ||    |  ||  ||                        |
Db    1090  GAGGTCTTCTCCCACGGGAAGTACATGCAGAGCACCACAGTGGAGCAGTCCCACACCAAG  1149

Qy    1194  TGGACTACTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGC---  1250
              |||      ||||  |||||| |  |||| || |||||  ||    |||   |    ||
Db    1150  TGGGTGCGCTATAATGGCCCGGTACCCAAGCCGCGGCCTGGAGCGTGCATCGACAGCGAG  1209

Qy    1251  ---------------------------CCCTCCTCTGATAAGGCCCTGACCTTCATG  1280
                                       |   | ||  |||  |  |||    ||| |
Db    1210  GCACGGGCCGCCAACTACACCAGCTCCTTGAATTTGCCAGACAAGACGCTGCAGTTCGTT  1269

Qy    1281  AAGGACCATTTCCTGATGGATGA---------GCAAGTGGTGGGGACGCCCCTGCTGGTG  1331
              ||  |||||      ||||||||||       |  |  |      |  ||||   |   |
Db    1270  AAAGACCACCCTTTGATGGATGACTCGGTAACCCCAATAGACAACAGGCCCAGGTTAATC  1329

Qy    1332  AAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCCTTGATGGGCAC  1391
              ||     |   |||  |  ||  ||  |  |  |  |||||      |||||| |||  ||||||
Db    1330  AAGAAAGATGTGAACTACACCCAGATCGTGGTGGACCGGACCCAGGCCCTGGATGGGAGT  1389

Qy    1392  AGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGGCTGTGGTAAGT  1451
                |  ||  ||||||||      |   |  ||     |   ||  |  ||  |||||  ||    |         ||
Db    1390  GTCTATGATGTCATGTTTGTCAGCACAGACCGGGGGAGCTCTGCACAAAGCCATC---AGC  1446

Qy    1452  GGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACCCTGAACCTGTT  1511
                ||     |  ||  |||   |  |  || ||||   |||||  ||||    |||    |||  ||  ||
Db    1447  CTCGAGCACGCTGTTCACATCATCGAGGAGACCCAGCTCTTCCAGGACTTTGAGCCAGTC  1506

Qy    1512  CGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGT------AGGCTTCTCAGGA  1565
              |  |  |||||  ||||  |   | |  ||||       ||||||          ||||
Db    1507  CAGACCCTGCTGCTGTCTTCAAAGAAGGGCAACAGGTTTGTCTATGCTGGCTCTAACTCG  1566

Qy    1566  GGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTC  1625
              || ||         || |||  |    |||   |||| |        | |   | ||| |  ||||||||
Db    1567  GGCGTGGTCCAGGCCCCGCTGGCCTTCTGTGGGAAGCACGGCACCTGCGAGGACTGTGTG  1626

Qy    1626  CTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTG  1672
              || ||  |||||||||| ||||  ||||||   |||          |||||
Db    1627  CTGGCGCGGGACCCCTACTGCGCCTGGAGCCCGCCCACAGCGACCTG  1673
```

RESULT 3
US-09-077-940A-3
; Sequence 3, Application US/09077940A
; Patent No. 6576441
; GENERAL INFORMATION:
; APPLICANT: KIMURA, Toru et al.
; TITLE OF INVENTION: NOVEL SEMAPHORIN Z AND GENE ENCODING THE SAME
; FILE REFERENCE: 0020-4426P
; CURRENT APPLICATION NUMBER: US/09/077,940A
; CURRENT FILING DATE: 1998-06-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 3524
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:

  Query Match   4.0%;   Score 126; DB 4; Length 3524;
  Best Local Similarity   55.3%;   Pred. No. 2.5e-23;
  Matches 315; Conservative   0; Mismatches 240; Indels   15; Gaps   3;

```
Qy       450 AAGAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAAT 509
             | ||||   |   | |||    |||||  ||||||  |   || ||| |   |    |
Db       390 ATGAAGGGCAAACAGGAGGGCGAGTGTCGAAACTTCGTAAAGGTGCTGCTCCTTCGGGAC 449

Qy       510 GTCACCCATCTCTACACCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAA 569
             |   ||   ||||     |||||  ||  |||||||||| |||  |   ||  ||  |
Db       450 GAGTCCACGCTCTTTGTGTGCGGTTCCAACGCCTTCAACCCGGTGTGCGCCAACTACAGC 509

Qy       570 CTTCAAGATTCCTACCTGTTGCCCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAA 629
             |  |       |  ||||  |||| ||    ||  |         |||     || |  ||
Db       510 ATAGA------CACCCTGCAGCCCGTCGGAGACAA------CATCAGCGGTATGGCCCGC 557

Qy       630 AGCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCT 689
             |||| |  ||||||    |||      ||    ||  ||||    || |||||||||| |
Db       558 TGCCCGTACGACCCCAAGCACGCCAATGTTGCCCTCTTCTCTGACGGGATGCTCTTCACA 617

Qy       690 GGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAG 749
             | ||||  |   |  ||||||| | || |||   | || |   |||| || ||   | |
Db       618 GCTACTGTTACCGACTTCCTAGCCATTGATGCTGTCATCTACCGCAGCCTCGGGGACAGG 677

Qy       750 CCTGTCCTCAAGACCGACAACTTCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCA 809
             ||   |||      ||||  ||     |    |    |  |  |   | || | | ||||||
Db       678 CCCACCCTGCGCACCGTGAAACATGACTCCAAGTGGTTCAAAGAGCCTTACTTTGTCCAT 737

Qy       810 GCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGAC 869
             ||  |     | |    |   ||||||||||||||||||| |||||   || |  ||||||| ||
Db       738 GCGGTGGAGTGGGGGCAGCCATGTCTACTTCTTCTTCCGGGAGATTGCGATGGAGTTTAAC 797

Qy       870 TTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGC 929
             | | |||| | |      || || ||||| |||| |||||||| ||||||| |||||||| |||
Db       798 TACCTGGAGAAGGTGGTGGTGTCCCGCGTGGCCCGAGTGTGCAAGAACGACGTGGGAGGC 857

Qy       930 GAAAAGC---TGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCCAGCTGCTCTGCACC 986
             |   ||||| |||||| ||||||| |||||||||||||||||| | ||| |||| |
Db       858 TCCCCCCGCGTGCTGGAGAAGCAGTGGACGTCCTTCCTGAAGGCGCGGCTCAACTGCTCT 917

Qy       987 CAGCCGGGGCAGCTGCCCTTCAACGTCATC 1016
             || || |   |   ||| || || ||| |
Db       918 GTACCCGGAGACTCCCATTTCTACTTCAAC 947
```


RESULT 4

US-09-077-940A-1
; Sequence 1, Application US/09077940A
; Patent No. 6576441
; GENERAL INFORMATION:
; APPLICANT: KIMURA, Toru et al.
; TITLE OF INVENTION: NOVEL SEMAPHORIN Z AND GENE ENCODING THE SAME
; FILE REFERENCE: 0020-4426P
; CURRENT APPLICATION NUMBER: US/09/077,940A
; CURRENT FILING DATE: 1998-06-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 3692
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
;   FEATURE:
;   NAME/KEY: 5'UTR
;   LOCATION: (1)..(18)
;   OTHER INFORMATION:
;   NAME/KEY: CDS
;   LOCATION: (19)..(2682)
;   OTHER INFORMATION:
;   NAME/KEY: 3'UTR
;   LOCATION: (2683)..(3653)
;   OTHER INFORMATION:
;   NAME/KEY: polyA_site
;   LOCATION: (3654)..(3692)
;   OTHER INFORMATION:
US-09-077-940A-1

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     Query Match              4.0%;   Score 125.4;   DB 4;   Length 3692;
     Best Local Similarity    58.5%;  Pred. No. 3.7e-23;
     Matches  238;  Conservative    0;  Mismatches  166;  Indels   3;  Gaps    1;

Qy      611 CATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGT 670
                |||     || |   | ||   ||||||| |||||| ||    ||   || ||  ||||
Db      522 CATCAGTGGTATGGCCCGCTGCCCCTACGACCCCAAGCATGCCAATGTCGCCCTCTTCTC 581

Qy      671 GGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGAT 730
                ||||||||||||  | |  || | |   ||||||| | || || |  |   |
Db      582 AGATGGGATGCTCTTCACAGCCACAGTAACTGACTTCCTAGCCATCGACGCTGTTATCTA 641

Qy      731 GCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCTGGCTGCATCA 790
                || |  || ||   ||  ||| ||   || ||   || | |   | | ||  | |
Db      642 CCGTAGCCTTGGGGACCGGCCCACACTGCGCACAGTAAAGCATGACTCCAAGTGGTTTAA 701

Qy      791 TGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGA 850
                || | |  |||||||   || |     | |          |||||||||||||||||  |||
Db      702 AGAGCCATACTTTGTGCATGCGGTGGAGTGGGGAAGCCACGTCTACTTCTTCTTCCGGGA 761

Qy      851 GACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTG 910
                ||  ||||  ||||||  |||   | || | | |            || || ||||| | || ||
Db      762 GATCGCCATGGAGTTTAACTATCTGGAAAAGGTGGTGGTGTCCCGTGTGGCCCGTGTATG 821

Qy      911 CAAGAATGACGTGGGCGG---CGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAA 967
                |||||||| |||||||||  |   |     | ||||| ||||| |||||||   |||||||||
Db      822 CAAGAATGATGTGGGCGGCTCCCCACGGGTGCTGGAGAAGCAGTGGACTTCCTTCCTGAA 881
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Qy      968  GGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCA 1014
             |||||  |||   |||| ||  ||| ||| |   |  |  |||| ||  |||
Db      882  GGCCCGGCTCAACTGCTCCGTGCCTGGGGACTCACACTTCTACTTCA 928


RESULT 5
US-09-976-594-1002
; Sequence 1002, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
;   APPLICANT: Furness, Michael
;   APPLICANT:  Buchbinder, Jenny
;   TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH
STEROIDS
;   FILE REFERENCE: PA-0041 US
;   CURRENT APPLICATION NUMBER: US/09/976,594
;   CURRENT FILING DATE:  2001-10-12
;   PRIOR APPLICATION NUMBER: 60/240,409
;   PRIOR FILING DATE: 2000-10-12
;   NUMBER OF SEQ ID NOS: 1143
;   SOFTWARE: PERL Program
; SEQ ID NO 1002
;   LENGTH: 2278
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6673549 411373.7
US-09-976-594-1002

  Query Match                3.2%;   Score 102;  DB 4;   Length 2278;
  Best Local Similarity    50.0%;   Pred. No. 4.9e-17;
  Matches  339;  Conservative    0;  Mismatches  330;  Indels    9;  Gaps     3;

Qy      618  GGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATGGG 677
             ||||  |  |  |  |||| | ||| ||  ||       |  ||  |  || |  |||||
Db      761  GGAATGGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACTGTTTGCAGATGGA 820

Qy      678  ATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATGCGCACA 737
             |  || || || || |  ||  ||| | |||||| | || |||  | || |  |  || |
Db      821  AAACTATACTCAGCCACAGTGACTGACTTCCTTGCCATTGACGCAGTCATTTACCGGAGT 880

Qy      738  CTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCTGGCTGCATCATGACGCC 797
             || |||      ||| |||  ||||| |||  |         |  |  | || |
Db      881  CTTGGAGAAAGCCCTACCCTGCGGACCGTCAAGCACGATTCAAAATGGTTGAAAGAACCA 940

Qy      798  TCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGACAGCC 857
             | ||||||| |||| |  ||| |   |       |||||||||||||| ||| | |||
Db      941  TACTTTGTTCAAGCCGTGGATTACGGAGATTATATCTACTTCTTCTTCAGGGAAATAGCA 1000

Qy      858  AGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAGAAT 917
             |||| | || | | | ||| |         |  | |||||||  || || ||||||
Db     1001  GTGGAGTATAACACCATGGGAAAGGTAGTTTTCCCAAGAGTGGCTCAGGTTTGTAAGAAT 1060

Qy      918  GACGTGGGCGG---CGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCCAG 974
             || |||| ||      ||| | ||| |||| |||||||| | ||||||||||||||| |
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Db     1061 GATATGGGAGGATCTCAAAGAGTCCTGGAGAAACAGTGGACGTCGTTCCTGAAGGCGCGC 1120

Qy      975 CTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGGTCCTGCTC 1034
             || ||||| |     || || |    | || | ||| | || || |
Db     1121 TTGAACTGCTCAGTTCCTGGAGACTCTCATTTTTATTTCAACATTCTCCAGGCAGTTACA 1180

Qy     1035 CCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCTCCCAGTGGCAGGTT 1094
              |    | | | || | |  | |  | |   | |   || |        |     |
Db     1181 GATGTGATTCGTATCAACGGGCGTGATGT---TGTCCTGGCAACGTTTTCTACACCTTAT 1237

Qy     1095 GGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACATTGAACGTGTCTTT 1154
              | | |    | ||||| || |||||||     |  | ||||||| |||| |||
Db     1238 AACAGCATCCCTGGGTCTGCAGTCTGTGCCTATGACATGCTTGACATTGCCAGTGTTTTT 1297

Qy     1155 AAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTAC---TTATAGGGGC 1211
             |  |||| || ||| ||    |||        |||   |||||| |   |   |   |
Db     1298 ACTGGGAGATTCAAGGAACAGAAGTCTCCTGATTCCACCTGGACACCAGTTCCTGATGAA 1357

Qy     1212 CCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTGATAAGGCCCTG 1271
             | |   | || ||| |||||||| | || | |        |||||| || |
Db     1358 CGAGTTCCTAAGCCCAGGCCAGGTTGCTGTGCTGGCTCATCCTCCTTAGAAAGATATGCA 1417

Qy     1272 ACCTTCATGAAGGACCAT 1289
             |||| ||   || || |
Db     1418 ACCTCCAATGAGTTCCCT 1435


RESULT 6
US-09-833-381-202
; Sequence 202, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
;  APPLICANT: Robison, Keith E.
;  TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
;  FILE REFERENCE: 5800-119
;  CURRENT APPLICATION NUMBER: US/09/833,381
;  CURRENT FILING DATE: 2001-04-11
;  PRIOR APPLICATION NUMBER: 09/516,448
;  PRIOR FILING DATE: 2000-02-29
;  NUMBER OF SEQ ID NOS: 2050
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 202
;   LENGTH: 121
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-833-381-202

  Query Match            3.1%;   Score 98.6;  DB 4;  Length 121;
  Best Local Similarity  88.4%;  Pred. No. 9e-17;
  Matches  107;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy      794 CGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAGAC 853
             |||||||||||||| || ||||||||| ||||| | || ||||||||||||| |||||||
Db        1 CGCCTCCTTTGTGGAAGACATCCCTTCTACCCACGGCGCCTACTTCTTCTTCCAGGAGAC 60

Qy      854 AGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAA 913
             |||||||||||| ||||   |||||||||||||||||||   || ||||||||||||||||
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Db        61 AGCCAGCGAGTTAGACTCTTTTGAGAGGCTCCACACATAATGGTTGGCTAGAGTCTGCAA 120

Qy       914 G 914
             |
Db       121 G 121


RESULT 7
US-09-254-594-5
; Sequence 5, Application US/09254594
; Patent No. 6566094
; GENERAL INFORMATION:
;  APPLICANT:  KIMURA, Toru
;  APPLICANT:  KIKUCHI, Kaoru
;  TITLE OF INVENTION:   NOVEL SEMAPHORIN GENE: SEMAPHORIN Y
;  FILE REFERENCE:   0020-4527P
;  CURRENT APPLICATION NUMBER: US/09/254,594
;  CURRENT FILING DATE: 1999-05-11
;  NUMBER OF SEQ ID NOS:   13
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 5
;   LENGTH: 2790
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: ()..()
;   OTHER INFORMATION: Tissue Type: Child Brain
;   NAME/KEY: CDS
;   LOCATION: (1)..(2790)
;   OTHER INFORMATION: Identification Method: E
;   NAME/KEY: misc_feature
;   LOCATION: ()..()
;   OTHER INFORMATION: Identification Method: P for resulting peptide
US-09-254-594-5

  Query Match              3.1%;   Score 98.6;  DB 4;  Length 2790;
  Best Local Similarity   50.1%;   Pred. No. 4.3e-16;
  Matches  369;  Conservative    0;  Mismatches  344;  Indels   24;  Gaps    4;

Qy       472 AGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCG 531
             |||| | ||||| || ||||| || ||| | |   |   |    ||| |||| |
Db       359 AGTGCTACAACTATATTCGTGTTCTTGTTCCCTGGGACTCCCAGACGCTCCTTGCCTGTG 418

Qy       532 GCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGC 591
             | || | | |||||||||| || | | || |              | ||
Db       419 GAACGAACTCATTCAGCCCTGTGTGCCGCAGCTATGGGAT-----------AACTTCGC 466

Qy       592 CCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACA 651
                    ||||| ||| || || | | | | ||||||||||| || | ||
Db       467 TGCAGCAGGAGGGTGAGGAACTGAGTGGGCAGGCTCGATGCCCCTTTGATGCCACCCAGT 526

Qy       652 AGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGG 711
               |   ||| ||||| | || || | || || || | |||| ||         | ||||| ||
Db       527 CCAACGTGGCCATCTTTGCAGAGGGCAGCCTGTACTCAGCCACAGCTGCGGATTTCCAGG 586

Qy       712 GCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACT 771
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           |||||| | | |    | | || ||  |||||||   |||    ||| ||| |
Db    587 CCAGTGATGCTGTAGTTTACAGAAGCCTTGGGCCCCAGCCCCCACTCCGCTCCGCCAAGT 646

Qy    772 TCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCG 831
           | | | | || | || |   |||||| ||| |         | |
Db    647 ATGACTCCAAGTGGCTCCGAGAGCCACACTTTGTCCAGGCCTTGGAGCATGGAGACCATG 706

Qy    832 TCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACAT 891
           |||||||||||||| |||   | ||| ||   | | || | | ||   |
Db    707 TCTACTTCTTCTTCCGCGAGGTCTCTGTGGAGGATGCTCGGCTGGGGAAGGTGCAGTTCT 766

Qy    892 CGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTG---CTGCAGAAGA 948
           | || || ||  |||| || ||  |||| ||||||||     | |     || |
Db    767 CCCGCGTAGCCCGAGTATGTAAACGTGACATGGGCGGCTCGCCTCGGGCCTTGGACCGCC 826

Qy    949 AGTGGACCACCTTCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCA 1008
           | |||||  ||||||||||| | |||    |||| |    || ||| |     | |||
Db    827 ACTGGACATCCTTCCTGAAGCTTCGGCTCAACTGCTCTGTCCCTGGGGACTCTACTTTCT 886

Qy   1009 A---CGTCATCCGCCACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCT 1065
           |    | | |    || || |      || | | |     |         |     |||
Db    887 ATTTGATGTTTTACAGGCCTTGACTGGGCCTGTGAACCTGCATGGCCGCTCTGCTCTCT 946

Qy   1066 ACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCT 1125
           |  |||||||||| |||||    |         | | |  ||||||| || || ||||
Db    947 TTGGGGTCTTCACCACCCAGACCAA------TAGCATCCCTGGCTCTGCCGTCTGCGCCT 1000

Qy   1126 TCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAA 1185
           ||| ||  || ||||| ||||  ||| |||| || | ||| ||| || ||
Db   1001 TCTACCTGGATGAGATTGAGCGTGGGTTTGAGGGCAAGTTCAAGGAGCAGAGGAGTCTGG 1060

Qy   1186 CTTCACGCTGGACTACT 1202
           |      |||||||| ||
Db   1061 ATGGGGCCTGGACTCCT 1077
```

RESULT 8
US-09-254-594-4
; Sequence 4, Application US/09254594
; Patent No. 6566094
; GENERAL INFORMATION:
; APPLICANT: KIMURA, Toru
; APPLICANT: KIKUCHI, Kaoru
; TITLE OF INVENTION: NOVEL SEMAPHORIN GENE: SEMAPHORIN Y
; FILE REFERENCE: 0020-4527P
; CURRENT APPLICATION NUMBER: US/09/254,594
; CURRENT FILING DATE: 1999-05-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
;   LENGTH: 3432
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: ()..()
;   OTHER INFORMATION: Tissue Type: Child Brain

```
   Query Match          3.1%;   Score 98.6;  DB 4;   Length 3432;
   Best Local Similarity   50.1%;   Pred. No. 4.8e-16;
   Matches  369;  Conservative    0;  Mismatches  344;  Indels   24;  Gaps    4;

Qy        472 AGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCG 531
              |||| | ||||| || ||||| || ||| | |   |    |     ||| |    |||| |
Db        546 AGTGCTACAACTATATTCGTGTTCTTGTTCCCTGGGACTCCCAGACGCTCCTTGCCTGTG 605

Qy        532 GCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGC 591
              | || | | |||||||||| || | | | || |               | ||
Db        606 GAACGAACTCATTCAGCCCTGTGTGCCGCAGCTATGGGAT-----------AACTTCGC 653

Qy        592 CCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACA 651
              |||||     |||    ||    ||    | |   | | |||||||||| || | ||
Db        654 TGCAGCAGGAGGGTGAGGAACTGAGTGGGCAGGCTCGATGCCCCTTTGATGCCACCCAGT 713

Qy        652 AGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGG 711
              |   |||  ||||| |  || || | || || || | | ||          | |||| ||
Db        714 CCAACGTGGCCATCTTTGCAGAGGGCAGCCTGTACTCAGCCACAGCTGCGGATTTCCAGG 773

Qy        712 GCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACT 771
              ||||||  | | | |       | | || ||  |||||||   |||   ||| |||| |
Db        774 CCAGTGATGCTGTAGTTTACAGAAGCCTTGGGCCCCAGCCCCCACTCCGCTCCGCCAAGT 833

Qy        772 TCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCG 831
              | | | | || | || | | ||||||      |||    | |             | |
Db        834 ATGACTCCAAGTGGCTCCGAGAGCCACACTTTGTCCAGGCCTTGGAGCATGGAGACCATG 893

Qy        832 TCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACAT 891
              |||||||||||||||| |||    |   |   ||| ||  | | || | | | |      |
Db        894 TCTACTTCTTCTTCCGCGAGGTCTCTGTGGAGGATGCTCGGCTGGGGAAGGTGCAGTTCT 953

Qy        892 CGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTG---CTGCAGAAGA 948
              | || || || |||| || || || ||||  ||||||||  | | |     || |
Db        954 CCCGCGTAGCCCGAGTATGTAAACGTGACATGGGCGGCTCGCCTCGGGCCTTGGACCGCC 1013

Qy        949 AGTGGACCACCTTCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCA 1008
              | |||||  |||||||||| ||| ||||| |   || |   || ||| |    | |||
Db       1014 ACTGGACATCCTTCCTGAAGCTTCGGCTCAACTGCTCTGTCCCTGGGGACTCTACTTTCT 1073

Qy       1009 A---CGTCATCCGCCACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCT 1065
              |   | |   | | || || |       || | |       |      |      |||
Db       1074 ATTTTGATGTTTTACAGGCCTTGACTGGGCCTGTGAACCTGCATGGCCGCTCTGCTCTCT 1133
```

```
Qy     1066 ACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCT 1125
               |  |||||||||  |||||        |         |  |      ||||||| || || ||||
Db     1134 TTGGGGTCTTCACCACCCAGACCAA------TAGCATCCCTGGCTCTGCCGTCTGCGCCT 1187

Qy     1126 TCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAA 1185
               |||   ||      ||  |||||  ||||    |||  ||||  || |  |||  |||   ||    |
Db     1188 TCTACCTGGATGAGATTGAGCGTGGGTTTGAGGGCAAGTTCAAGGAGCAGAGGAGTCTGG 1247

Qy     1186 CTTCACGCTGGACTACT 1202
               |        |||||||| ||
Db     1248 ATGGGGCCTGGACTCCT 1264


RESULT 9
US-09-254-594-2
; Sequence 2, Application US/09254594
; Patent No. 6566094
; GENERAL INFORMATION:
;  APPLICANT: KIMURA, Toru
;  APPLICANT: KIKUCHI, Kaoru
;  TITLE OF INVENTION:   NOVEL SEMAPHORIN GENE: SEMAPHORIN Y
;  FILE REFERENCE:   0020-4527P
;  CURRENT APPLICATION NUMBER: US/09/254,594
;  CURRENT FILING DATE:  1999-05-11
;  NUMBER OF SEQ ID NOS:   13
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 2787
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: ()..()
;   OTHER INFORMATION: Tissue Type: Brain
;   NAME/KEY: CDS
;   LOCATION: (1)..(2787)
;   OTHER INFORMATION: Identification Method: E
;   NAME/KEY: misc_feature
;   LOCATION: ()..()
;   OTHER INFORMATION: Identification Method: P for resulting peptide
US-09-254-594-2

   Query Match              2.9%;   Score 89.8;  DB 4;  Length 2787;
   Best Local Similarity   50.1%;  Pred. No. 9.5e-14;
   Matches  369; Conservative   0;  Mismatches  347;  Indels   21;  Gaps    5;

Qy      472 AGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCG 531
               |  || | ||||| |||||||||| || ||| | |      |         |||     |||| |
Db      356 AATGCTACAACTACATCCGTGTTCTTGTTCCCTGGGACTCGCAGACACTCCTTGCCTGTG 415

Qy      532 GCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGC 591
               |  ||         |||||||||||||| |||  |  |  |  ||   |     |  |    | |
Db      416 GAACAAATTCCTTCAGCCCTGTGTGTCGCAGCTATGGGATAACATCTCTGCAAC------ 469

Qy      592 CCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACA 651
               |||||   |||   ||  ||  ||  |||   | | |||||||||||| || | ||
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Db      470  ------AGGAGGGTGAGGAGCTGAGTGGGCAAGCTCGATGCCCCTTTGATGCCACCCAGT 523

Qy      652  AGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGG 711
                |  |||  |||  |  || || |   | || || |  ||       |  |||| ||
Db      524  CCACTGTGGCCATCTCTGCAGAGGGTAGTTTGTACTCAGCCACAGCAGCAGATTTCCAGG 583

Qy      712  GCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACT 771
                |||||| |  |   |     || |  || ||| | |||||    |||    |  | ||  |
Db      584  CCAGTGATGCTGTGGTTTACAGAAGCCTTGGACCTCAGCCCCCACTCCGTTCTGCAAAGT 643

Qy      772  TCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCAT---CCCTTCGACCCAGG 828
                |  |  |  ||  || ||  || |     ||||||    ||  |    |   |||| |
Db      644  ATGACTCCAAGTGGCTTCGAGAGCCACACTTTGTCTATGCTTTGGAGCATGGAGACCATG 703

Qy      829  TCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACA 888
                || || |||  |     ||| || |      |   |     |  | | ||| | | ||
Db      704  TCTACTTCTTTCTTCCGGAGAAGTCTCTGTGGAGGACGCCCGGCCTGGGGAGGGTGCAGT 763

Qy      889  CATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTG---CTGCAGA 945
                ||  |||||||||   |  || || || ||     |||| |||| |||  |   |  || |
Db      764  TTTCCCGGGTGGCCCGGGTGTGTAAACGTGACATGGGTGGCTCACCACGGGCCTTGGATC 823

Qy      946  AGAAGTGGACCACCTTCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCT 1005
                |  |||||  |||||||  |||   ||  |||| || ||  || | |   |||
Db      824  GCCACTGGACATCCTTCCTTAAGCTGAGGCTCAACTGCTCCGTCCCTGGGGACTCTACCT 883

Qy     1006  TCAACGTCATCCGCCACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCT 1065
                || || |    |  |   | |||||   |  |||  |  | ||   |    | | | |
Db      884  TCTAC-TTTGATGTCTTACAGTCCTTAACTGGGCCTGTGAACCTGCATGGGCGCTCTGC- 941

Qy     1066  ACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCT 1125
                 |   |    ||  |||    |||   | |    |  ||||| || || || |||
Db      942  -CCTCTTTGGGGTCTTCACTACTCAGACCAATAGCATTCCTGGGTCTGCAGTCTGCGCCT 1000

Qy     1126  TCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAA 1185
                |||  ||   ||||||||||||| |||| |||| |||| || | ||| |||  || |
Db     1001  TCTACCTAGATGACATTGAACGTGGCTTTGAGGGCAAGTTCAAGGAGCAGAGGAGTCTGG 1060

Qy     1186  CTTCACGCTGGACTACT 1202
                |      |||||||| ||
Db     1061  ATGGGGCCTGGACTCCT 1077
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RESULT 10
US-09-254-594-1
; Sequence 1, Application US/09254594
; Patent No. 6566094
; GENERAL INFORMATION:
; APPLICANT: KIMURA, Toru
; APPLICANT: KIKUCHI, Kaoru
; TITLE OF INVENTION: NOVEL SEMAPHORIN GENE: SEMAPHORIN Y
; FILE REFERENCE: 0020-4527P
; CURRENT APPLICATION NUMBER: US/09/254,594
; CURRENT FILING DATE: 1999-05-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1

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  Query Match              2.9%;   Score 89.8;   DB 4;   Length 3195;
  Best Local Similarity   50.1%;   Pred. No. 1e-13;
  Matches  369;  Conservative    0;  Mismatches  347;  Indels  21;  Gaps    5;


Qy      472 AGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCG 531
                | || | ||||| |||||||||| || ||| | |     |       ||| |||| |
Db      406 AATGCTACAACTACATCCGTGTTCTTGTTCCCTGGGACTCGCAGACACTCCTTGCCTGTG 465


Qy      532 GCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGC 591
              | ||       |||||||||||| ||| | | | || | | | | | | |
Db      466 GAACAAATTCCTTCAGCCCTGTGTGTCGCAGCTATGGGATAACATCTCTGCAAC------ 519


Qy      592 CCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACA 651
                      ||||| ||| || || ||| | | ||||||||| || | ||
Db      520 ------AGGAGGGTGAGGAGCTGAGTGGGCAAGCTCGATGCCCCTTTGATGCCACCCAGT 573


Qy      652 AGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGG 711
              |   ||| ||| |  || ||  |   || || |  ||        | |||| ||
Db      574 CCACTGTGGCCATCTCTGCAGAGGGTAGTTTGTACTCAGCCACAGCAGCAGATTTCCAGG 633


Qy      712 GCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACT 771
              ||||||  |  |  |        || || ||| | |||||      |||      || |
Db      634 CCAGTGATGCTGTGGTTTACAGAAGCCTTGGACCTCAGCCCCCACTCCGTTCTGCAAAGT 693


Qy      772 TCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCAT---CCCTTCGACCCAGG 828
              | |  |  || || ||  || | |  ||||||| ||  | |     | |     ||| |
Db      694 ATGACTCCAAGTGGCTTCGAGAGCCACACTTTGTCTATGCTTTGGAGCATGGAGACCATG 753


Qy      829 TCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACA 888
              || || ||| |    ||| || |     |    |   | | | |||| | ||
Db      754 TCTACTTCTTTCTTCCGGAGAAGTCTCTGTGGAGGACGCCCGGCCTGGGGAGGGTGCAGT 813


Qy      889 CATCGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTG---CTGCAGA 945
              || |||||||| | | ||  || ||     |||| |||| |||  | | |   || |
Db      814 TTTCCCGGGTGGCCCGGGTGTGTAAACGTGACATGGGTGGCTCACCACGGGCCTTGGATC 873


Qy      946 AGAAGTGGACCACCTTCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCT 1005
              | ||||| |||||| ||| |||     ||| |||| || || ||| | |||    |||
Db      874 GCCACTGGACATCCTTCCTTAAGCTGAGGCTCAACTGCTCCGTCCCTGGGGACTCTACCT 933
```

```
Qy    1006 TCAACGTCATCCGCCACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCT 1065
           || || |     | |   | ||||| |   ||| |  ||  ||   | || |
Db     934 TCTAC-TTTGATGTCTTACAGTCCTTAACTGGGCCTGTGAACCTGCATGGGCGCTCTGC- 991

Qy    1066 ACGCAGTCTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCT 1125
           |     |      || |       |||        | |    | ||||| || || ||||
Db     992 -CCTCTTTGGGGTCTTCACTACTCAGACCAATAGCATTCCTGGGTCTGCAGTCTGCGCCT 1050

Qy    1126 TCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAA 1185
           |||  ||   |||||||||||||| |||| |||| |||| || | ||| |||  ||   |
Db    1051 TCTACCTAGATGACATTGAACGTGGCTTTGAGGGCAAGTTCAAGGAGCAGAGGAGTCTGG 1110

Qy    1186 CTTCACGCTGGACTACT 1202
           |     |||||||| ||
Db    1111 ATGGGGCCTGGACTCCT 1127


RESULT 11
US-09-976-594-632
; Sequence 632, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
;  APPLICANT: Furness, Michael
;  APPLICANT:  Buchbinder, Jenny
;  TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH
STEROIDS
;  FILE REFERENCE: PA-0041 US
;  CURRENT APPLICATION NUMBER: US/09/976,594
;  CURRENT FILING DATE:  2001-10-12
;  PRIOR APPLICATION NUMBER: 60/240,409
;  PRIOR FILING DATE: 2000-10-12
;  NUMBER OF SEQ ID NOS: 1143
;  SOFTWARE: PERL Program
; SEQ ID NO 632
;   LENGTH: 4286
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6673549 238322.6
US-09-976-594-632

  Query Match             2.7%;  Score 84.2;  DB 4;  Length 4286;
  Best Local Similarity  50.3%;  Pred. No. 3.6e-12;
  Matches  273;  Conservative   0;  Mismatches  253;  Indels   17;  Gaps    2;

Qy     472 AGTGTTTCAACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCG 531
           |||| | ||||| || ||||| || ||| | |  |  |      ||| |    |||| |
Db     611 AGTGCTACAACTATATTCGTGTTCTTGTTCCCTGGGACTCCCAGACGCTCCTTGCCTGTG 670

Qy     532 GCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGC 591
           | ||   | | |||||||||||| ||  |  | | || |                | ||
Db     671 GAACGAACTCATTCAGCCCTGTGTGCCGCAGCTATGGGAT-----------AACTTCGC 718

Qy     592 CCATCTCGGAGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACA 651
             |||| |   ||| ||  ||  ||  |.|  | | ||||||||||| || | ||
```

```
Db     719 TGCAGCAGGAGGGTGAGGAACTGAGTGGGCAGGCTCGATGCCCCTTTGATGCCACCCAGT 778

Qy     652 AGCATACGGCTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGG 711
               |   |||  |||| |  || || |  || || || |  ||        |  |||| ||
Db     779 CCAACGTGGCCATCTTTGCAGAGGGCAGCCTGTACTCAGCCACAGCTGCGGATTTCCAGG 838

Qy     712 GCAGTGAGCCCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACT 771
               ||||||  |  |  |      || | || || |||||||   |||   ||| ||| |
Db     839 CCAGTGATGCTGTAGTTTACAGAAGCCTTGGGCCCCAGCCCCCACTCCGCTCCGCCAAGT 898

Qy     772 TCCTCCGCTGGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCG 831
               |  |  | ||  |  || |      ||||||   ||| |          |       |
Db     899 ATGACTCCAAGTGGCTCCGAGAGCCACACTTTGTCCAGGCCTTGGAGCATGGAGACCATG 958

Qy     832 TCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACAT 891
               ||||||||||||||||   |||     |       ||| ||   | | |||| | ||    |
Db     959 TCTACTTCTTCTTCCGCGAGGTCTCTGTGGAGGATGCTCGGCTGGGGAGGGTGCAGTTCT 1018

Qy     892 CGCGGGTGGCTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGA--- 948
               | ||  || || ||  |||| || ||    |||| ||||||||||      |   |     |
Db    1019 CCCGCGTAGCCCGAGTATGTAAACGTGACATGGGCGGCTCGCCTTCGGGTCTTGGTACCG 1078

Qy     949 --AGTGGACCACCTTCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTT 1006
               |  |||||  ||||||||||||     | |||     |||| |       || ||| |       | ||
Db    1079 CCACTGGACATCCTTCCTGAAGCTTCGGCTCAACTGCTCTGTCCCTGGGGACTCTACTTT 1138

Qy    1007 CAA 1009
               | |
Db    1139 CTA 1141


RESULT 12
US-08-121-713D-59
; Sequence 59, Application US/08121713D
; Patent No. 5639856
;   GENERAL INFORMATION:
;     APPLICANT:  Goodman, Corey S.
;     APPLICANT:  Kolodkin, Alex L.
;     APPLICANT:  Matthes, David
;     APPLICANT:  Bentley, David R.
;     APPLICANT:  O'Connor, Timothy
;     TITLE OF INVENTION:  The Semaphorin Gene Family
;     NUMBER OF SEQUENCES:  100
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  SCIENCE & TECHNOLOGY LAW GROUP
;       STREET:  268 Bush Street, Suite 3200
;       CITY:  San Francisco
;       STATE:  CA
;       COUNTRY:  USA
;       ZIP:  94104
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/121,713D
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;   INFORMATION FOR SEQ ID NO: 59:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 3560 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 1..1953
US-08-121-713D-59

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  Query Match              2.5%;   Score 78.6;  DB 1;  Length 3560;
  Best Local Similarity   49.2%;   Pred. No. 1e-10;
  Matches  358;  Conservative   0;  Mismatches  324;  Indels  45;  Gaps    4;


Qy        612 ATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTG 671
              | | | ||| | |       |||||| || ||  |||||| || |||| |||
Db        139 AAGAACGGACAGGCGGTGTGCCCCTACGATCCACGTCACAACTCCACCTCTGTGCTGGCC 198


Qy        672 GATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATG 731
              ||         ||  |||||| |||||| ||    | |||    |||||  || || || |
Db        199 GACAACGAACTGTATTCCGGTACCGTGGCGGATTTCAGTGGCAGCGATCCGATTATC--- 255


Qy        732 CGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCTGGCTGCATCAT 791
                          | || |     ||| |||||||  | | |  ||     | |    |  |
Db        256 ------------TACCGGGAGCCCCTGCAGACCGAGCAGTACGATAGCCTAAGTCTCAAC 303


Qy        792 GACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAG 851
              |  |   | |||||||||      |  |    |  | |  | ||||| ||||||||  |||
Db        304 GCACCGAACTTTGTGAGCTCATTTACGCAGGGCGACTTTGTCTATTTCTTCTTTCGGGAA 363


Qy        852 ACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGC 911
              || |||  |||||| |  | || || | |          ||||| || ||  | ||||||
Db        364 ACCGCCGTTGAGTTTATCAACTGTGGCAAGGCGATTTATTCGCGCGTTGCCCGCGTCTGC 423


Qy        912 AAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCC 971
              ||     |||   || ||| | |   | |   | | |  ||||| ||||||| ||| ||
Db        424 AAATGGGACAAAGGTGGCCCGCATCGATTCCGCAACCGCTGGACATCCTTCCTCAAGTCC 483


Qy        972 CAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCA----------------TC 1016
              |  ||  |||| ||  || || | |   || ||| || | |                  |
Db        484 CGCCTCAACTGCTCCATTCCCGGCGATTATCCTTTCTACTTTAATGAAATCCAATCTGCC 543


Qy       1017 CGCCACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTC 1076
              || |   ||| |   |   |    | ||    |     | |      |||||||| |||||||
Db        544 AGCAATCTGGTGGAGGGACAGTATGGCTCGATGAGCTCGAAACTGATCTACGGAGTCTTC 603
```

```
Qy      1077 ACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTG 1136
             | | | | | |   |     |   |      |||| ||||||||||||||  |  ||| |
Db       604 AACACGCCGAGCAA------CTCAATTCCCGGCTCAGCGGTTTGTGCCTTTGCCCTCCAG 657

Qy      1137 GACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTG- 1195
             |||||||      |   ||| ||||  |  |  ||| |||  ||         |  ||  |||
Db       658 GACATTGCCGATACGTTTGAGGGTCAGTTCAAGGAGCAGACTGGCATCAACTCCAACTGG 717

Qy      1196 --------GACTACTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTG 1247
                     || |     | ||  || ||  |    ||| |  |  |       |        |
Db       718 CTGCCAGTGAACAACGCCAAGGTACCCGATCCTCGACCCGGTTCCTGTCACAACGATTCG 777

Qy      1248 GGCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAA 1307
              |  |     | |||    |  |||| ||||| ||   |||| || |||||| ||| |
Db       778 AGAGCGCTTCCGGATCCCACACTGAACTTCATCAAAACACATTCGCTAATGGACGAGAAT 837

Qy      1308 GTGGTGG 1314
             ||| ||
Db       838 GTGCCGG 844
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RESULT 13
US-08-835-268-59
; Sequence 59, Application US/08835268
; Patent No. 5807826
;   GENERAL INFORMATION:
;   APPLICANT: Goodman, Corey S.
;   APPLICANT: Kolodkin, Alex L.
;   APPLICANT: Matthes, David
;   APPLICANT: Bentley, David R.
;   APPLICANT: O'Connor, Timothy
;   TITLE OF INVENTION: The Semaphorin Gene Family
;   NUMBER OF SEQUENCES: 100
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
;   STREET: 268 Bush Street, Suite 3200
;   CITY: San Francisco
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94104
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/835,268
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/121,713
;   FILING DATE: 13-SEP-1993
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Osman, Richard A.
;   REGISTRATION NUMBER: 36,627
;   REFERENCE/DOCKET NUMBER: B94-002-1
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    Query Match              2.5%;   Score 78.6;  DB 1;  Length 3560;
    Best Local Similarity   49.2%;   Pred. No. 1e-10;
    Matches  358;  Conservative    0;  Mismatches  324;  Indels  45;  Gaps    4;
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Qy     612 ATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTG 671
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Db     139 AAGAACGGACAGGCGGTGTGCCCCTACGATCCACGTCACAACTCCACCTCTGTGCTGGCC 198

Qy     672 GATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATG 731
               ||       || |||||| |||||  ||    | |||  ||||| || || || |
Db     199 GACAACGAACTGTATTCCGGTACCGTGGCGGATTTCAGTGGCAGCGATCCGATTATC--- 255

Qy     732 CGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCTGGCTGCATCAT 791
                        | || |    ||| |||||||| | | |      ||      |  |
Db     256 ------------TACCGGGAGCCCCTGCAGACCGAGCAGTACGATAGCCTAAGTCTCAAC 303

Qy     792 GACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAG 851
               |   |     |||||||       |   |   |   | | |  | |||||  ||||||||  |||
Db     304 GCACCGAACTTTGTGAGCTCATTTACGCAGGGCGACTTTGTCTATTTCTTCTTTCGGGAA 363

Qy     852 ACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGC 911
               || |||   ||||||  |  || ||  | |         ||||| || ||  | ||||||
Db     364 ACCGCCGTTGAGTTTATCAACTGTGGCAAGGCGATTTATTCGCGCGTTGCCCGCGTCTGC 423

Qy     912 AAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCC 971
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Db     424 AAATGGGACAAAGGTGGCCCGCATCGATTCCGCAACCGCTGGACATCCTTCCTCAAGTCC 483

Qy     972 CAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCA---------------TC 1016
               |  ||   |||| ||   || ||  |  || ||| || | |                 |
Db     484 CGCCTCAACTGCTCCATTCCCGGCGATTATCCTTTCTACTTTAATGAAATCCAATCTGCC 543

Qy    1017 CGCCACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTC 1076
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Db     544 AGCAATCTGGTGGAGGGACAGTATGGCTCGATGAGCTCGAAACTGATCTACGGAGTCTTC 603

Qy    1077 ACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTG 1136
               | | | | |    | |   |  ||| ||||||||||||||| | ||| |
Db     604 AACACGCCGAGCAA------CTCAATTCCCGGCTCAGCGGTTTGTGCCTTTGCCCTCCAG 657

Qy    1137 GACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTG- 1195
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Db    658 GACATTGCCGATACGTTTGAGGGTCAGTTCAAGGAGCAGACTGGCATCAACTCCAACTGG 717

Qy   1196 --------GACTACTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTG 1247
              || |      | ||  || ||  |    ||| |  |  |       |      |
Db    718 CTGCCAGTGAACAACGCCAAGGTACCCGATCCTCGACCCGGTTCCTGTCACAACGATTCG 777

Qy   1248 GGCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAA 1307
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Db    778 AGAGCGCTTCCGGATCCCACACTGAACTTCATCAAAACACATTCGCTAATGGACGAGAAT 837

Qy   1308 GTGGTGG 1314
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Db    838 GTGCCGG 844


RESULT 14
US-09-060-692-59
; Sequence 59, Application US/09060692
; Patent No. 5935865
;   GENERAL INFORMATION:
;     APPLICANT:  Goodman, Corey S.
;     APPLICANT:  Kolodkin, Alex L.
;     APPLICANT:  Matthes, David
;     APPLICANT:  Bentley, David R.
;     APPLICANT:  O'Connor, Timothy
;     TITLE OF INVENTION:  The Semaphorin Gene Family
;     NUMBER OF SEQUENCES:  100
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  SCIENCE & TECHNOLOGY LAW GROUP
;       STREET:  268 Bush Street, Suite 3200
;       CITY:  San Francisco
;       STATE:  CA
;       COUNTRY:  USA
;       ZIP:  94104
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/060,692
;       FILING DATE:
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/121,713
;       FILING DATE:  13-SEP-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Osman, Richard A.
;       REGISTRATION NUMBER:  36,627
;       REFERENCE/DOCKET NUMBER:  B94-002-1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415)343-4341
;       TELEFAX:  (415) 343-4342
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  59:
;     SEQUENCE CHARACTERISTICS:
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  Query Match                2.5%;   Score 78.6;  DB 2;  Length 3560;
  Best Local Similarity     49.2%;   Pred. No. 1e-10;
   Matches  358;  Conservative   0;  Mismatches  324;  Indels  45;  Gaps   4;


Qy        612 ATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTG 671
              | | | ||| | |      |||||| || || || |||||  ||  |||| |||
Db        139 AAGAACGGACAGGCGGTGTGCCCCTACGATCCACGTCACAACTCCACCTCTGTGCTGGCC 198


Qy        672 GATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGCCCATCCTGATG 731
              ||        || ||||| ||||| ||   |  |||    ||||| || || || |
Db        199 GACAACGAACTGTATTCCGGTACCGTGGCGGATTTCAGTGGCAGCGATCCGATTATC--- 255


Qy        732 CGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCTGGCTGCATCAT 791
                        | || |    ||| |||||||| | | |   ||          |   |
Db        256 -----------TACCGGGAGCCCCTGCAGACCGAGCAGTACGATAGCCTAAGTCTCAAC 303


Qy        792 GACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAG 851
              |  |    |||||||     | | |   | | | |  | ||||| |||||||    |||
Db        304 GCACCGAACTTTGTGAGCTCATTTACGCAGGGCGACTTTGTCTATTTCTTCTTTCGGGAA 363


Qy        852 ACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGC 911
              || |||  ||||||  | || ||  | |      ||||| || || | ||||||
Db        364 ACCGCCGTTGAGTTTATCAACTGTGGCAAGGCGATTTATTCGCGCGTTGCCCGCGTCTGC 423


Qy        912 AAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCC 971
              ||    |||    || |||   | |  | | |      ||||| ||||||| ||| ||
Db        424 AAATGGGACAAAGGTGGCCCGCATCGATTCCGCAACCGCTGGACATCCTTCCTCAAGTCC 483


Qy        972 CAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCA---------------TC 1016
              |  ||   |||| ||  || || | |  || ||| || | |                 |
Db        484 CGCCTCAACTGCTCCATTCCCGGCGATTATCCTTTCTACTTTAATGAAATCCAATCTGCC 543


Qy       1017 CGCCACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTC 1076
              || |   ||| | |  | | | | || |  || |     ||||||| |||||| |||||||
Db        544 AGCAATCTGGTGGAGGGACAGTATGGCTCGATGAGCTCGAAACTGATCTACGGAGTCTTC 603


Qy       1077 ACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTG 1136
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Db        604 AACACGCCGAGCAA------CTCAATTCCCGGCTCAGCGGTTTGTGCCTTTGCCCTCCAG 657


Qy       1137 GACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTG- 1195
              |||||||      |   ||| |||| | | ||| ||| ||          |  ||   |||
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Qy       1196 --------GACTACTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTG 1247
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Qy   1308 GTGGTGG 1314
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Db    838 GTGCCGG 844
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RESULT 15
US-08-833-391-59
; Sequence 59, Application US/08833391
; Patent No. 6013781
;   GENERAL INFORMATION:
;   APPLICANT: Goodman, Corey S.
;   APPLICANT: Kolodkin, Alex L.
;   APPLICANT: Matthes, David
;   APPLICANT: Bentley, David R.
;   APPLICANT: O'Connor, Timothy
;   TITLE OF INVENTION: The Semaphorin Gene Family
;   NUMBER OF SEQUENCES: 100
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
;   STREET: 268 Bush Street, Suite 3200
;   CITY: San Francisco
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94104
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/833,391
;   FILING DATE:
;   CLASSIFICATION: 530
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/121,713
;   FILING DATE: 13-SEP-1993
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Osman, Richard A.
;   REGISTRATION NUMBER: 36,627
;   REFERENCE/DOCKET NUMBER: B94-002-1
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415)343-4341
;   TELEFAX: (415) 343-4342
;   TELEX:
;   INFORMATION FOR SEQ ID NO: 59:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 3560 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   FEATURE:
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        Query Match            2.5%;   Score 78.6;  DB 3;  Length 3560;
        Best Local Similarity  49.2%;  Pred. No. 1e-10;
        Matches  358;  Conservative   0;  Mismatches  324;  Indels  45;  Gaps   4;

Qy      612 ATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTG 671
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Db      139 AAGAACGGACAGGCGGTGTGCCCCTACGATCCACGTCACAACTCCACCTCTGTGCTGGCC 198

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                       | || |     ||| ||||||| | | | ||       | |
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Qy      792 GACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCTTCGAGGAG 851
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Qy      852 ACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGGCTAGAGTCTGC 911
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Db      424 AAATGGGACAAAGGTGGCCCGCATCGATTCCGCAACCGCTGGACATCCTTCCTCAAGTCC 483

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Qy      1248 GGCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAA 1307
              | |    | |||   | |||| |||||||||| ||   |||| || ||||| ||| |
Db       778 AGAGCGCTTCCGGATCCCACACTGAACTTCATCAAAACACATTCGCTAATGGACGAGAAT 837

Qy      1308 GTGGTGG 1314
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Db       838 GTGCCGG 844


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Job time : 222 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 13, 2004, 09:44:40 ; Search time 1271 Seconds
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Perfect score: 3143
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Scoring table: IDENTITY_NUC
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Searched: 2947324 seqs, 2269024515 residues

Total number of hits satisfying chosen parameters: 5894648

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                         %
Result   Query

No.	Score	Match	Length	DB	ID	Description
1	3143	100.0	3143	10	US-09-946-374-276	Sequence 276, App
2	3143	100.0	3143	12	US-10-015-395A-276	Sequence 276, App
3	3143	100.0	3143	13	US-10-006-485A-276	Sequence 276, App
4	3143	100.0	3143	13	US-10-013-907A-276	Sequence 276, App
5	3143	100.0	3143	13	US-10-015-499A-276	Sequence 276, App
6	3143	100.0	3143	13	US-10-226-254A-276	Sequence 276, App
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37	3143	100.0	3143	15	US-10-017-867A-276	Sequence 276, App
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ALIGNMENTS

RESULT 1
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; Sequence 276, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
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; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
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;  PRIOR APPLICATION NUMBER: 60/102487
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   Best Local Similarity  100.0%;  Pred. No. 0;
   Matches 3143;  Conservative   0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy        1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60
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Qy      301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360
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Db      301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360

Qy      361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420
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Qy     421 GTGACAGAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480
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Qy     481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540
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Qy     541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600
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Db     541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600

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Qy     661 CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC 720
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Qy     781 GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT 840
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Db     781 GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT 840

Qy     841 TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG 900
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Qy     961 TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC 1020
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Db     961 TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC 1020

Qy    1021 ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT 1080
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Qy    1081 CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA 1140
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Qy    1141 TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA 1200
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Db    1201 CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG 1260
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Qy    1261 ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC 1320
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Db    1261 ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC 1320

Qy    1321 CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC 1380
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Db    1381 TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG 1440

Qy    1441 CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC 1500
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Qy    1501 CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT 1560
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Qy    1561 CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT 1620
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Db    1561 CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT 1620

Qy    1621 GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680
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Db    1621 GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680

Qy    1681 TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740
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Db    1681 TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740

Qy    1741 CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800
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Db    1741 CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800

Qy    1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860
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Db    1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860

Qy    1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920
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Db    1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920

Qy    1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980
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Qy    1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040
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Db    1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040

Qy    2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100
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Db    2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100
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Qy    2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160
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Qy    2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220
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Qy    2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280
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Db    2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280

Qy    2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340
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Qy    2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400
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Db    2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400

Qy    2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460
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Db    2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460

Qy    2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520
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Qy    2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580
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Qy    2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640
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Db    2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640

Qy    2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700
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Qy    2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760
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Qy    2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820
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Qy    2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940
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Db    2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940

Qy    2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000
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Qy     3001   CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060
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Qy     3061   TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120
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Qy     3121   TAAAAATATAAGGCTTAAAAAAA 3143
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Db     3121   TAAAAATATAAGGCTTAAAAAAA 3143
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RESULT 2
US-10-015-395A-276
; Sequence 276, Application US/10015395A
; Publication No. US20040073015A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C57
; CURRENT APPLICATION NUMBER: US/10/015,395A
; CURRENT FILING DATE: 2001-12-12
; Prior application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 276
;   LENGTH: 3143
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-015-395A-276

  Query Match   100.0%; Score 3143; DB 12; Length 3143;
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Qy        1   GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60
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Db        1   GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60

Qy       61   ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120
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Qy    121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180
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Qy    301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360
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Db    301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360

Qy    361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420
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Qy    421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480
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Qy    481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540
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Qy    601 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660
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Qy    661 CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC 720
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Qy    721 CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT 780
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Qy    781 GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT 840
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Db    781 GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT 840

Qy    841 TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG 900
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Db    841 TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG 900

Qy    901 CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT 960
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Qy     1141  TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA 1200
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Qy     1261  ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC 1320
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Db     1261  ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC 1320

Qy     1321  CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC 1380
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Db     1321  CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC 1380

Qy     1381  TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG 1440
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Db     1681  TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740

Qy     1741  CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800
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Db     1741  CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800
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Qy   1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860
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Qy    2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700
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Db    2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700

Qy    2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760
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RESULT 3
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; Publication No. US20030064062A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C9
; CURRENT APPLICATION NUMBER: US/10/006,485A
; CURRENT FILING DATE: 2001-12-06
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Qy        1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60

Qy       61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120

Qy      121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180

Qy      181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240

Qy      241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300

Qy      301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360

Qy      361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420

Qy      421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480

Qy      481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540

Qy      541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600

Qy      601 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660
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                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601  AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG  660

Qy      661  CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC  720
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661  CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC  720

Qy      721  CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT  780
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721  CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT  780

Qy      781  GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT  840
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781  GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT  840

Qy      841  TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  900
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841  TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  900

Qy      901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960

Qy      961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020

Qy     1021  ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT  1080
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021  ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT  1080

Qy     1081  CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA  1140
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081  CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA  1140

Qy     1141  TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA  1200
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141  TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA  1200

Qy     1201  CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG  1260
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201  CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG  1260

Qy     1261  ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC  1320
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1261  ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC  1320

Qy     1321  CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC  1380
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1321  CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC  1380

Qy     1381  TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG  1440
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1381  TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG  1440

Qy     1441  CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC  1500
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1441 CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC 1500

Qy   1501 CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT 1560

Qy   1561 CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT 1620

Qy   1621 GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680

Qy   1681 TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740

Qy   1741 CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800
          |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800

Qy   1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860

Qy   1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920

Qy   1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980

Qy   1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040

Qy   2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100

Qy   2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160

Qy   2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220

Qy   2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280

Qy   2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340
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Qy    2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400

Qy    2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460

Qy    2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520

Qy    2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580

Qy    2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640

Qy    2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700

Qy    2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760

Qy    2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820

Qy    2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880

Qy    2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940

Qy    2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000

Qy    3001 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3001 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060

Qy    3061 TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3061 TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120

Qy    3121 TAAAAATATAAGGCTTAAAAAAA 3143
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Db    3121 TAAAAATATAAGGCTTAAAAAAA 3143
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RESULT 4
US-10-013-907A-276
; Sequence 276, Application US/10013907A
; Publication No. US20030064925A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C34
; CURRENT APPLICATION NUMBER: US/10/013,907A
; CURRENT FILING DATE: 2001-12-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 276
;   LENGTH: 3143
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-013-907A-276

    Query Match   100.0%; Score 3143; DB 13; Length 3143;
    Best Local Similarity 100.0%; Pred. No. 0;
    Matches 3143; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60

Qy   61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120

Qy   121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180

Qy   181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240

Qy   241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300

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Qy    301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360

Qy    361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420

Qy    421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480

Qy    481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540

Qy    541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600

Qy    601 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660

Qy    661 CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC 720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC 720

Qy    721 CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT 780
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT 780

Qy    781 GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT 840
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT 840

Qy    841 TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG 900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG 900

Qy    901 CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT 960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT 960

Qy    961 TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC 1020
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC 1020

Qy   1021 ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT 1080
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT 1080

Qy   1081 CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA 1140
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA 1140

Qy   1141 TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA 1200
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                        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141    TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA 1200

Qy      1201    CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG 1260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201    CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG 1260

Qy      1261    ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC 1320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261    ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC 1320

Qy      1321    CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC 1380
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321    CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC 1380

Qy      1381    TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG 1440
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381    TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG 1440

Qy      1441    CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC 1500
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1441    CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC 1500

Qy      1501    CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT 1560
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1501    CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT 1560

Qy      1561    CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT 1620
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1561    CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT 1620

Qy      1621    GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1621    GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680

Qy      1681    TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1681    TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740

Qy      1741    CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1741    CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800

Qy      1801    AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1801    AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860

Qy      1861    TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1861    TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920

Qy      1921    ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1921    ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980

Qy      1981    CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    1981  CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA  2040

Qy    2041  CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA  2100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2041  CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA  2100

Qy    2101  CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA  2160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2101  CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA  2160

Qy    2161  CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC  2220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2161  CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC  2220

Qy    2221  CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG  2280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2221  CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG  2280

Qy    2281  AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG  2340
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2281  AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG  2340

Qy    2341  CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA  2400
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2341  CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA  2400

Qy    2401  CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC  2460
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2401  CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC  2460

Qy    2461  TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC  2520
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2461  TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC  2520

Qy    2521  TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC  2580
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2521  TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC  2580

Qy    2581  TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC  2640
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2581  TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC  2640

Qy    2641  TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC  2700
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2641  TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC  2700

Qy    2701  CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA  2760
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2701  CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA  2760

Qy    2761  TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG  2820
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2761  TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG  2820

Qy    2821  AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC  2880
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2821  AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC  2880
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Qy    2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940

Qy    2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000

Qy    3001 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3001 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060

Qy    3061 TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3061 TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120

Qy    3121 TAAAAATATAAGGCTTAAAAAAA 3143
           |||||||||||||||||||||||
Db    3121 TAAAAATATAAGGCTTAAAAAAA 3143
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RESULT 5
US-10-015-499A-276
; Sequence 276, Application US/10015499A
; Publication No. US20030065142A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C42
; CURRENT APPLICATION NUMBER: US/10/015,499A
; CURRENT FILING DATE: 2001-12-11
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 276
;   LENGTH: 3143
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-015-499A-276

   Query Match   100.0%; Score 3143; DB 13; Length 3143;
   Best Local Similarity   100.0%; Pred. No. 0;
   Matches 3143; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy     1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60

Qy    61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120

Qy   121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180

Qy   181 TGCCGACGACGACCGCGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TGCCGACGACGACCGCGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240

Qy   241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300

Qy   301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360

Qy   361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420

Qy   421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480

Qy   481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540

Qy   541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600

Qy   601 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660

Qy   661 CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC 720

Qy   721 CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT 780

Qy   781 GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT 840
```

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Qy    841  TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  900

Qy    901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960

Qy    961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC 1020
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC 1020

Qy   1021  ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT 1080
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT 1080

Qy   1081  CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA 1140
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA 1140

Qy   1141  TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA 1200
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA 1200

Qy   1201  CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG 1260
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG 1260

Qy   1261  ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC 1320
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261  ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC 1320

Qy   1321  CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC 1380
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321  CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC 1380

Qy   1381  TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG 1440
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381  TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG 1440

Qy   1441  CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC 1500
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441  CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC 1500

Qy   1501  CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT 1560
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501  CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT 1560

Qy   1561  CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT 1620
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561  CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT 1620

Qy   1621  GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621  GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680

Qy   1681  TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740
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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740

Qy    1741 CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800

Qy    1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860

Qy    1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920

Qy    1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980

Qy    1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040

Qy    2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100

Qy    2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160

Qy    2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220

Qy    2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280

Qy    2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340

Qy    2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400

Qy    2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460

Qy    2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520

Qy    2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db     2521  TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580

Qy     2581  TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2581  TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640

Qy     2641  TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2641  TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700

Qy     2701  CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2701  CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760

Qy     2761  TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2761  TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820

Qy     2821  AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2821  AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880

Qy     2881  TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2881  TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940

Qy     2941  CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2941  CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000

Qy     3001  CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3001  CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060

Qy     3061  TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3061  TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120

Qy     3121  TAAAAATATAAGGCTTAAAAAAA 3143
             |||||||||||||||||||||||
Db     3121  TAAAAATATAAGGCTTAAAAAAA 3143
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RESULT 6
US-10-226-254A-276
; Sequence 276, Application US/10226254A
; Publication No. US20030224478A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

    Query Match   100.0%; Score 3143; DB 13; Length 3143;
    Best Local Similarity 100.0%; Pred. No. 0;
    Matches 3143; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60

Qy   61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120

Qy   121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180

Qy   181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240

```
Qy    241  CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA  300

Qy    301  CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG  360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG  360

Qy    361  CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA  420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA  420

Qy    421  GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA  480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA  480

Qy    481  ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG  540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG  540

Qy    541  CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG  600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG  600

Qy    601  AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG  660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG  660

Qy    661  CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC  720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC  720

Qy    721  CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT  780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT  780

Qy    781  GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT  840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT  840

Qy    841  TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  900

Qy    901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960

Qy    961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC 1020

Qy   1021  ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT 1080
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Qy    1081  CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA  1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081  CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA  1140

Qy    1141  TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA  1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141  TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA  1200

Qy    1201  CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG  1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201  CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG  1260

Qy    1261  ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC  1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261  ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC  1320

Qy    1321  CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC  1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321  CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC  1380

Qy    1381  TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG  1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381  TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG  1440

Qy    1441  CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC  1500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441  CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC  1500

Qy    1501  CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT  1560
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501  CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT  1560

Qy    1561  CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT  1620
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561  CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT  1620

Qy    1621  GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC  1680
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621  GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC  1680

Qy    1681  TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG  1740
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681  TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG  1740

Qy    1741  CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA  1800
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741  CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA  1800

Qy    1801  AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT  1860
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801  AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT  1860

Qy    1861  TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT  1920
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861  TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT  1920

Qy    1921  ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG  1980
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                         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980

Qy     1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040

Qy     2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100

Qy     2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160

Qy     2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220

Qy     2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280

Qy     2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340

Qy     2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400

Qy     2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460

Qy     2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520

Qy     2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580

Qy     2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640

Qy     2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700

Qy     2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760

Qy     2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820

Qy    2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880

Qy    2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940

Qy    2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000

Qy    3001 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3001 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060

Qy    3061 TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3061 TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120

Qy    3121 TAAAAATATAAGGCTTAAAAAAA 3143
           |||||||||||||||||||||||
Db    3121 TAAAAATATAAGGCTTAAAAAAA 3143


RESULT 7
US-10-006-856A-276
; Sequence 276, Application US/10006856A
; Publication No. US20030044841A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C14
;  CURRENT APPLICATION NUMBER: US/10/006,856A
;  CURRENT FILING DATE:  2002-05-10
;  NUMBER OF SEQ ID NOS: 477
;  Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 276
;   LENGTH: 3143
;   TYPE: DNA
;   ORGANISM: Homo sapiens
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Query Match              100.0%;  Score 3143;  DB 15;  Length 3143;
Best Local Similarity    100.0%;  Pred. No. 0;
Matches 3143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy       1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60

Qy      61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120

Qy     121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180

Qy     181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240

Qy     241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300

Qy     301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360

Qy     361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420

Qy     421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480

Qy     481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540

Qy     541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600
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Db     541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600

Qy     601 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660

Qy     661 CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC 720

Qy     721 CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT 780
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Qy    781  GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT  840
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Db    781  GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT  840

Qy    841  TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  900

Qy    901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960

Qy    961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020
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Db    961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020

Qy   1021  ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT  1080
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Db   1021  ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT  1080

Qy   1081  CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA  1140
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA  1140

Qy   1141  TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA  1200
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA  1200

Qy   1201  CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG  1260
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG  1260

Qy   1261  ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC  1320
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261  ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC  1320

Qy   1321  CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC  1380
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321  CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC  1380

Qy   1381  TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG  1440
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Db   1381  TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG  1440

Qy   1441  CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC  1500
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Qy   1501  CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT  1560
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Db   1501  CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT  1560

Qy   1561  CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT  1620
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561  CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT  1620
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Qy   1621 GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680
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Db   1621 GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680

Qy   1681 TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740
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Db   1681 TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740

Qy   1741 CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800
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Db   1741 CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800

Qy   1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860
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Db   1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860

Qy   1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920
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Db   1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920

Qy   1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980
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Db   1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980

Qy   1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040

Qy   2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100
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Db   2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100

Qy   2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160
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Db   2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160

Qy   2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220
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Db   2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220

Qy   2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280
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Db   2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280

Qy   2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340
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Qy   2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400
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Db   2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400

Qy   2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460

Qy   2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520
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Db   2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520

Qy   2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580
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Db   2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580

Qy   2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640

Qy   2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700
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Db   2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700

Qy   2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760
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Qy   3061 TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120
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Db   3061 TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120

Qy   3121 TAAAAATATAAGGCTTAAAAAAA 3143
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Db   3121 TAAAAATATAAGGCTTAAAAAAA 3143
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RESULT 8
US-10-006-818A-276
; Sequence 276, Application US/10006818A
; Publication No. US20030054406A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.

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  Query Match            100.0%;  Score 3143;  DB 15;  Length 3143;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 3143;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy        1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60
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Db       61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120

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Qy      181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240
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Db      181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240

Qy      241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300
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Qy      301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360
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Db      301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360

Qy      361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420
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Db    421  GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA  480

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Qy    541  CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG  600
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Qy    601  AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG  660
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Qy    661  CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC  720
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Db    661  CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC  720

Qy    721  CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT  780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT  780

Qy    781  GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT  840
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Db    781  GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT  840

Qy    841  TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  900
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Qy    901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960
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Db    901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960

Qy    961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020

Qy   1021  ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT  1080
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Db   1141  TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA  1200

Qy   1201  CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG  1260
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Db   1201  CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG  1260

Qy   1261  ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC  1320
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Qy    1321 CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC 1380
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Qy    1621 GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680
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Db    1621 GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680

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Db    1681 TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740

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Qy    1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860
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Qy    1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920

Qy    1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980

Qy    1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040

Qy    2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100

Qy    2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160
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Qy   2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220

Qy   2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280

Qy   2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340

Qy   2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400

Qy   2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460

Qy   2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520

Qy   2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580

Qy   2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640

Qy   2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700

Qy   2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760

Qy   2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820

Qy   2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880

Qy   2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940

Qy   2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000

Qy   3001 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060
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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3001 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060

Qy     3061 TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3061 TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120

Qy     3121 TAAAAATATAAGGCTTAAAAAAA 3143
                    |||||||||||||||||||||||
Db     3121 TAAAAATATAAGGCTTAAAAAAA 3143
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RESULT 9
US-10-015-393A-276
; Sequence 276, Application US/10015393A
; Publication No. US20030069179A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C46
; CURRENT APPLICATION NUMBER: US/10/015,393A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 276
;   LENGTH: 3143
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-015-393A-276

   Query Match   100.0%; Score 3143; DB 15; Length 3143;
   Best Local Similarity   100.0%; Pred. No. 0;
   Matches 3143; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy        1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60

Qy       61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120

Qy      121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180
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              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180

Qy        181 TGCCGACGACGACCGCGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGCCGACGACGACCGCGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240

Qy        241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300

Qy        301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360

Qy        361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420

Qy        421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480

Qy        481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540

Qy        541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600

Qy        601 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660

Qy        661 CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC 720

Qy        721 CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT 780

Qy        781 GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT 840

Qy        841 TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG 900

Qy        901 CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT 960

Qy        961 TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020

Qy   1021  ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT  1080

Qy   1081  CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA  1140

Qy   1141  TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA  1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA  1200

Qy   1201  CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG  1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG  1260

Qy   1261  ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC  1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261  ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC  1320

Qy   1321  CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC  1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321  CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC  1380

Qy   1381  TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG  1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381  TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG  1440

Qy   1441  CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC  1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441  CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC  1500

Qy   1501  CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT  1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501  CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT  1560

Qy   1561  CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT  1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561  CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT  1620

Qy   1621  GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC  1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621  GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC  1680

Qy   1681  TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG  1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681  TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG  1740

Qy   1741  CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA  1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741  CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA  1800

Qy   1801  AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT  1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801  AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT  1860
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Qy    1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920

Qy    1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980

Qy    1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040

Qy    2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100

Qy    2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160

Qy    2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220

Qy    2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280

Qy    2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340

Qy    2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400

Qy    2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460
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Db    2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460

Qy    2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520
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Db    2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520

Qy    2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580

Qy    2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640
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Db    2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640

Qy    2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700
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Qy    2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760

Qy    2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820

Qy    2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880

Qy    2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940

Qy    2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000

Qy    3001 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3001 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060

Qy    3061 TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120
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Db    3061 TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120

Qy    3121 TAAAAATATAAGGCTTAAAAAAA 3143
           |||||||||||||||||||||||
Db    3121 TAAAAATATAAGGCTTAAAAAAA 3143
```

RESULT 10
US-10-015-869A-276
; Sequence 276, Application US/10015869A
; Publication No. US20030073130A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C45
; CURRENT APPLICATION NUMBER: US/10/015,869A
; CURRENT FILING DATE: 2002-06-25

Query Match   100.0%;   Score 3143;   DB 15;   Length 3143;
Best Local Similarity   100.0%;   Pred. No. 0;
Matches 3143;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy        1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60
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Db        1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60

Qy       61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120
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Qy      121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180
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Db      121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180

Qy      181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240
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Db      181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240

Qy      241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300

Qy      301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360

Qy      361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420

Qy      421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480

Qy      481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540

Qy      541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600
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Db      541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600

Qy      601 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660

Qy      661 CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC 720
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Db      661  CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC  720

Qy      721  CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT  780
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721  CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT  780

Qy      781  GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT  840
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781  GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT  840

Qy      841  TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  900
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841  TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  900

Qy      901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960

Qy      961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020

Qy     1021  ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT  1080
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Db     1021  ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT  1080

Qy     1081  CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA  1140
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081  CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA  1140

Qy     1141  TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA  1200
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141  TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA  1200

Qy     1201  CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG  1260
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201  CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG  1260

Qy     1261  ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC  1320
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1261  ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC  1320

Qy     1321  CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC  1380
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1321  CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC  1380

Qy     1381  TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG  1440
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1381  TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG  1440

Qy     1441  CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC  1500
                    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1441  CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC  1500

Qy     1501  CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT  1560
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Db    1501 CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT 1560

Qy    1561 CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT 1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT 1620

Qy    1621 GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680

Qy    1681 TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740
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Db    1681 TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740

Qy    1741 CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800
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Db    1741 CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800

Qy    1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860
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Db    1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860

Qy    1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920

Qy    1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980

Qy    1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040
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Db    1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040

Qy    2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100
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Db    2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100

Qy    2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160
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Db    2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160

Qy    2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220
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Db    2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220

Qy    2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280
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Db    2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280

Qy    2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340

Qy    2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400
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Qy   2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460
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Db   2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460

Qy   2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520
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Db   2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520

Qy   2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580
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Db   2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580

Qy   2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640

Qy   2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700
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Db   2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700

Qy   2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760
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Db   2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760

Qy   2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820
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Db   2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820

Qy   2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880
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Db   2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880

Qy   2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940

Qy   2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000
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Db   3001 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060

Qy   3061 TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120
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Db   3061 TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120

Qy   3121 TAAAAATATAAGGCTTAAAAAAA 3143
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Db   3121 TAAAAATATAAGGCTTAAAAAAA 3143
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RESULT 11
US-10-012-121A-276
; Sequence 276, Application US/10012121A

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   Query Match              100.0%;  Score 3143;  DB 15;  Length 3143;
   Best Local Similarity    100.0%;  Pred. No. 0;
   Matches 3143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60

Qy         61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120

Qy        121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180

Qy        181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240

Qy        241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300

Qy        301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360
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Qy    361  CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA  420
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Db    361  CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA  420

Qy    421  GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA  480
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Db    421  GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA  480

Qy    481  ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG  540
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Db    481  ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG  540

Qy    541  CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG  600
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Db    541  CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG  600

Qy    601  AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG  660
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Db    601  AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG  660

Qy    661  CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC  720
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Db    661  CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC  720

Qy    721  CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT  780
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Db    721  CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT  780

Qy    781  GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT  840
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Db    781  GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT  840

Qy    841  TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  900
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Db    841  TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  900

Qy    901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT  960

Qy    961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC  1020

Qy   1021  ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT  1080

Qy   1081  CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA  1140

Qy   1141  TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA  1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA  1200

Qy   1201  CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG  1260
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Db     1201  CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG  1260

Qy     1261  ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC  1320
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Db     1261  ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC  1320

Qy     1321  CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC  1380
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Db     1321  CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC  1380

Qy     1381  TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG  1440
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Db     1381  TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG  1440

Qy     1441  CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC  1500
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Db     1441  CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC  1500

Qy     1501  CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT  1560
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Db     1501  CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT  1560

Qy     1561  CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT  1620
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Db     1561  CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT  1620

Qy     1621  GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC  1680
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Db     1621  GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC  1680

Qy     1681  TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG  1740
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Db     1681  TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG  1740

Qy     1741  CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA  1800
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Db     1741  CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA  1800

Qy     1801  AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT  1860
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Db     1801  AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT  1860

Qy     1861  TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT  1920
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Db     1861  TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT  1920

Qy     1921  ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG  1980
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Db     1921  ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG  1980

Qy     1981  CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA  2040
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Db     1981  CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA  2040

Qy     2041  CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA  2100
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Qy    2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160
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Db    2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160

Qy    2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220
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Db    2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220

Qy    2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280
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Qy    2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400
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Db    2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460

Qy    2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520
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Qy    2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640
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Qy    2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700
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Db    2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700

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Qy    2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820
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Qy    2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940
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Qy    3061  TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120
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Db    3061  TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120

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RESULT 12
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; Sequence 276, Application US/10006116A
; Publication No. US20030082626A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan l.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2830P1C15
;  CURRENT APPLICATION NUMBER: US/10/006,116A
;  CURRENT FILING DATE:  2001-12-16
;  PRIOR APPLICATION NUMBER: 60/098716
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098723
;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098749
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;  PRIOR FILING DATE: 1998-09-01
;  PRIOR APPLICATION NUMBER: 60/098803
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;   PRIOR FILING DATE: 1998-09-17
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;   PRIOR FILING DATE: 1998-10-02
;   PRIOR APPLICATION NUMBER: 60/103258
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   Matches 3143;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy        1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60
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Qy       61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120
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Db       61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120

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Qy      181 TGCCGACGACGACCGCGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240
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Qy      241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300
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Qy      361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420
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Qy   1381  TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG  1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381  TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG  1440

Qy   1441  CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC  1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441  CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC  1500

Qy   1501  CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT  1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501  CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT  1560

Qy   1561  CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT  1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561  CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT  1620

Qy   1621  GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC  1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621  GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC  1680

Qy   1681  TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG  1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681  TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG  1740

Qy   1741  CATGTGCCAGTGGCCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA  1800
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                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1741   CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA   1800

Qy      1801   AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT   1860
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1801   AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT   1860

Qy      1861   TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT   1920
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1861   TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT   1920

Qy      1921   ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG   1980
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1921   ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG   1980

Qy      1981   CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA   2040
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1981   CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA   2040

Qy      2041   CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA   2100
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2041   CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA   2100

Qy      2101   CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA   2160
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2101   CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA   2160

Qy      2161   CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC   2220
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2161   CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC   2220

Qy      2221   CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG   2280
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2221   CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG   2280

Qy      2281   AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG   2340
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2281   AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG   2340

Qy      2341   CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA   2400
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2341   CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA   2400

Qy      2401   CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC   2460
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2401   CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC   2460

Qy      2461   TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC   2520
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2461   TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC   2520

Qy      2521   TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC   2580
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2521   TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC   2580

Qy      2581   TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC   2640
                   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db     2581  TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC  2640

Qy     2641  TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC  2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2641  TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC  2700

Qy     2701  CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA  2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2701  CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA  2760

Qy     2761  TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG  2820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2761  TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG  2820

Qy     2821  AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC  2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2821  AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC  2880

Qy     2881  TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA  2940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2881  TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA  2940

Qy     2941  CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG  3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2941  CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG  3000

Qy     3001  CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC  3060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3001  CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC  3060

Qy     3061  TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT  3120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     3061  TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT  3120

Qy     3121  TAAAAATATAAGGCTTAAAAAAA  3143
             |||||||||||||||||||||||
Db     3121  TAAAAATATAAGGCTTAAAAAAA  3143
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RESULT 13
US-10-006-117A-276
; Sequence 276, Application US/10006117A
; Publication No. US20030082627A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James

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     Query Match              100.0%;  Score 3143;  DB 15;  Length 3143;
     Best Local Similarity    100.0%;  Pred. No. 0;
     Matches 3143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;


Qy            1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60


Qy           61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120


Qy          121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180


Qy          181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240


Qy          241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300


Qy          301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360


Qy          361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420


Qy          421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480


Qy          481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540


Qy          541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    541  CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600

Qy    601  AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660

Qy    661  CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC 720

Qy    721  CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT 780

Qy    781  GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT 840

Qy    841  TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG 900

Qy    901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT 960

Qy    961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC 1020

Qy   1021  ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT 1080

Qy   1081  CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA 1140

Qy   1141  TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA 1200

Qy   1201  CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG 1260

Qy   1261  ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261  ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC 1320

Qy   1321  CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321  CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC 1380

Qy   1381  TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG 1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381  TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG 1440
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Qy    1441 CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC 1500
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC 1500

Qy    1501 CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT 1560
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT 1560

Qy    1561 CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT 1620
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT 1620

Qy    1621 GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680

Qy    1681 TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740

Qy    1741 CATGTGCCAGTGGCCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 CATGTGCCAGTGGCCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800

Qy    1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860

Qy    1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920

Qy    1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980

Qy    1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040

Qy    2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100

Qy    2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160
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Db    2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160

Qy    2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220

Qy    2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280
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```
Qy    2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340

Qy    2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400

Qy    2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460

Qy    2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520

Qy    2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580

Qy    2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640

Qy    2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820
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Db    2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820

Qy    2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880
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Qy    2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940
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; Sequence 276, Application US/10017527A
; Publication No. US20030082628A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan 1.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C63
; CURRENT APPLICATION NUMBER: US/10/017,527A
; CURRENT FILING DATE: 2001-12-13
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
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;  PRIOR APPLICATION NUMBER: 60/103396
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;  PRIOR FILING DATE: 1998-10-07
;  PRIOR APPLICATION NUMBER: 60/103449
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Best Local Similarity    100.0%;  Pred. No. 0;
Matches 3143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60
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Qy       61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120
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Qy      301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360
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Db   2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760

Qy   2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820
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Qy   2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880

Qy   2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940

Qy   2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000

Qy   3001 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060

Qy   3061 TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120

Qy   3121 TAAAAATATAAGGCTTAAAAAAA 3143
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Db   3121 TAAAAATATAAGGCTTAAAAAAA 3143
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RESULT 15
US-10-013-913A-276
; Sequence 276, Application US/10013913A
; Publication No. US20030083462A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C40
; CURRENT APPLICATION NUMBER: US/10/013,913A
; CURRENT FILING DATE: 2002-07-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 276
;   LENGTH: 3143
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-013-913A-276

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Query Match            100.0%;  Score 3143;  DB 15;  Length 3143;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches 3143;  Conservative   0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGC 60

Qy      61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 ATCCCCAGGCTCCAGAGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCC 120

Qy     121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TGGGCCTGGACCCCTGGAGCCTCCTGGGCCTTTTCCTCTTCCAACTGCTTCAGCTGCTGC 180

Qy     181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TGCCGACGACGACCGCGGGGGGGAGGCGGGCAGGGGCCCATGCCCAGGGTCAGATACTATG 240

Qy     241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA 300

Qy     301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CTCTGCTCCTGAGTGGTGATGGAAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGG 360

Qy     361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CCTTGGATATCCAGGATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCA 420

Qy     421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GTGACAGAAAAAAGAGTGAATGTGCCTTTAAGAAGAAGAGCAATGAGACACAGTGTTTCA 480

Qy     481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 ACTTCATCCGTGTCCTGGTTTCTTACAATGTCACCCATCTCTACACCTGCGGCACCTTCG 540

Qy     541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 CCTTCAGCCCTGCTTGTACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTCGG 600

Qy     601 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 AGGACAAGGTCATGGAGGGAAAAGGCCAAAGCCCCTTTGACCCCGCTCACAAGCATACGG 660

Qy     661 CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CTGTCTTGGTGGATGGGATGCTCTATTCTGGTACTATGAACAACTTCCTGGGCAGTGAGC 720

Qy     721 CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 CCATCCTGATGCGCACACTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCT 780

Qy     781 GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT 840
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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 GGCTGCATCATGACGCCTCCTTTGTGGCAGCCATCCCTTCGACCCAGGTCGTCTACTTCT 840

Qy      841 TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG 900
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 TCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG 900

Qy      901 CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT 960
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAGAAGTGGACCACCT 960

Qy      961 TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC 1020
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 TCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCC 1020

Qy     1021 ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT 1080
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 ACGCGGTCCTGCTCCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCT 1080

Qy     1081 CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA 1140
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081 CCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCTTCTCTCTCTTGGACA 1140

Qy     1141 TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA 1200
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141 TTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA 1200

Qy     1201 CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG 1260
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201 CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCTCCTCTG 1260

Qy     1261 ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC 1320
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1261 ATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGC 1320

Qy     1321 CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC 1380
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1321 CCCTGCTGGTGAAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAGACAGCCCAGGGCC 1380

Qy     1381 TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG 1440
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1381 TTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACAAGG 1440

Qy     1441 CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC 1500
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1441 CTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGGAAGAGATTCAGCTGTTCCCTGACC 1500

Qy     1501 CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT 1560
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1501 CTGAACCTGTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTTTGTAGGCTTCT 1560

Qy     1561 CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT 1620
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1561 CAGGAGGTGTCTGGAGGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACT 1620

Qy     1621 GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      1621 GTGTCCTTGCCCGGGACCCCCACTGTGCCTGGGACCCTGAGTCCCGAACCTGTTGCCTCC 1680

Qy      1681 TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1681 TGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGGGGAACCCAGAGTGGG 1740

Qy      1741 CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1741 CATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAAATCATTA 1800

Qy      1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1801 AAGAAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCACCTGTCAGCCT 1860

Qy      1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1861 TGGCCTCTTATTATTGGAGTCATGGCCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCT 1920

Qy      1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1921 ACAATGGCTCCCTCTTGCTGATAGTGCAGGATGGAGTTGGGGGTCTCTACCAGTGCTGGG 1980

Qy      1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1981 CAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCAGA 2040

Qy      2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2041 CCCTGGCCCTGGATCCTGAACTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA 2100

Qy      2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2101 CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCAGTCCTACTGGCCCCACTTTGTCA 2160

Qy      2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2161 CTGTCACTGTCCTCTTTGCCTTAGTGCTTTCAGGAGCCCTCATCATCCTCGTGGCCTCCC 2220

Qy      2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2221 CATTGAGAGCACTCCGGGCTCGGGGCAAGGTTCAGGGCTGTGAGACCCTGCGCCCTGGGG 2280

Qy      2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2281 AGAAGGCCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGGAATGCAGGACCTCTG 2340

Qy      2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2341 CCAGTGATGTGGACGCTGACAACAACTGCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA 2400

Qy      2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2401 CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCACAGCCC 2460

Qy      2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2461 TGACTAGGATGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTAC 2520
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Qy   2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580
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Db   2521 TCTGCATCACTGATGACACTCAGCAGGGTGATGCACAGCAGTCTGCCTCCCCTATGGGAC 2580

Qy   2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 TCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCCCCAGACCTGCTCC 2640

Qy   2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700
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Db   2641 TACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTC 2700

Qy   2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760
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Db   2701 CAGAAACACAGTGTTTCAAGAGACCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAA 2760

Qy   2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 TGAACACCAAACATCTAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTG 2820

Qy   2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880
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Db   2821 AAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCATGCAGGGATCTGCTCCC 2880

Qy   2881 TCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGA 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CCACCTTTCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG 3000

Qy   3001 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCC 3060
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 TCCCTTTTCCTTTGTTTTGGGATTCAGAAAACTGCTTGTCAGAGACTGTTTATTTTTTAT 3120

Qy   3121 TAAAAATATAAGGCTTAAAAAAA 3143
          |||||||||||||||||||||||
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Search completed: May 13, 2004, 22:44:40
Job time : 1283 secs
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